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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	CL000841
First Inventor	LUDUNGA et al
Title	ISOLATED HUMAN SECRETED
Express Mail Label No.	

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

- ☒ Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)
- ☐ Applicant claims small entity status.
See 37 CFR 1.27.
- ☒ Specification [Total Pages 63]
(preferred arrangement set forth below)
 - Descriptive title of the invention
 - Cross Reference to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to sequence listing, a table, or a computer program listing appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
- ☒ Drawing(s) (35 U.S.C. 113) [Total Sheets 43]
- Oath or Declaration [Total Pages]
 - ☐ Newly executed (original or copy)
 - ☐ Copy from a prior application (37 CFR 1.63 (d))
(for continuation/divisional with Box 17 completed)
 - ☐ **DELETION OF INVENTOR(S)**
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b)
- ☐ Application Data Sheet. See 37 CFR 1.76

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ACCOMPANYING APPLICATION PARTS

- ☐ Assignment Papers (cover sheet & document(s))
- ☐ 37 CFR 3.73(b) Statement of Attorney (when there is an assignee)
- ☐ English Translation Document (if applicable)
- ☐ Information Disclosure Statement (IDS)/PTO-1449
- ☐ Preliminary Amendment
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CL000841

ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND USES THEREOF

RELATED APPLICATIONS

The present application claims priority to provisional application U.S. Serial No. (To Be Assigned), filed October 27, 2000 (Atty. Docket CL000841-PROV).

FIELD OF THE INVENTION

The present invention is in the field of secreted proteins that are related to the retinoic acid receptor responder secreted subfamily, recombinant DNA molecules, and protein production. The present invention specifically provides novel peptides and proteins that effect protein phosphorylation and nucleic acid molecules encoding such peptide and protein molecules, all of which are useful in the development of human therapeutics and diagnostic compositions and methods.

BACKGROUND OF THE INVENTION

Secreted Proteins

Many human proteins serve as pharmaceutically active compounds. Several classes of human proteins that serve as such active compounds include hormones, cytokines, cell growth factors, and cell differentiation factors. Most proteins that can be used as a pharmaceutically active compound fall within the family of secreted proteins. It is, therefore, important in developing new pharmaceutical compounds to identify secreted proteins that can be tested for activity in a variety of animal models. The present invention advances the state of the art by providing many novel human secreted proteins.

Secreted proteins are generally produced within cells at rough endoplasmic reticulum, are then exported to the golgi complex, and then move to secretory vesicles or granules, where they are secreted to the exterior of the cell via exocytosis.

Secreted proteins are particularly useful as diagnostic markers. Many secreted proteins are found, and can easily be measured, in serum. For example, a 'signal sequence trap' technique can often be utilized because many secreted proteins, such as certain secretory breast cancer proteins, contain a molecular signal sequence for cellular export. Additionally, antibodies against particular secreted serum proteins can serve as potential diagnostic agents, such as for diagnosing cancer.

Secreted proteins play a critical role in a wide array of important biological processes in humans and have numerous utilities; several illustrative examples are discussed herein. For example, fibroblast secreted proteins participate in extracellular matrix formation. Extracellular matrix affects growth factor action, cell adhesion, and cell growth. Structural and quantitative characteristics of fibroblast secreted proteins are modified during the course of cellular aging and such aging related modifications may lead to increased inhibition of cell adhesion, inhibited cell stimulation by growth factors, and inhibited cell proliferative ability (Eleftheriou *et al.*, *Mutat Res* 1991 Mar-Nov;256(2-6):127-38).

The secreted form of amyloid beta/A4 protein precursor (APP) functions as a growth and/or differentiation factor. The secreted form of APP can stimulate neurite extension of cultured neuroblastoma cells, presumably through binding to a cell surface receptor and thereby triggering intracellular transduction mechanisms. (Roch *et al.*, *Ann N Y Acad Sci* 1993 Sep 24;695:149-57). Secreted APPs modulate neuronal excitability, counteract effects of glutamate on growth cone behaviors, and increase synaptic complexity. The prominent effects of secreted APPs on synaptogenesis and neuronal survival suggest that secreted APPs play a major role in the process of natural cell death and, furthermore, may play a role in the development of a wide variety of neurological disorders, such as stroke, epilepsy, and Alzheimer's disease (Mattson *et al.*, *Perspect Dev Neurobiol* 1998; 5(4):337-52).

Breast cancer cells secrete a 52K estrogen-regulated protein (see Rochefort *et al.*, *Ann N Y Acad Sci* 1986;464:190-201). This secreted protein is therefore useful in breast cancer diagnosis.

Two secreted proteins released by platelets, platelet factor 4 (PF4) and beta-thromboglobulin (betaTG), are accurate indicators of platelet involvement in hemostasis

and thrombosis and assays that measure these secreted proteins are useful for studying the pathogenesis and course of thromboembolic disorders (Kaplan, *Adv Exp Med Biol* 1978;102:105-19).

Vascular endothelial growth factor (VEGF) is another example of a naturally secreted protein. VEGF binds to cell-surface heparan sulfates, is generated by hypoxic endothelial cells, reduces apoptosis, and binds to high-affinity receptors that are up-regulated by hypoxia (Asahara *et al.*, *Semin Interv Cardiol* 1996 Sep;1(3):225-32).

Many critical components of the immune system are secreted proteins, such as antibodies, and many important functions of the immune system are dependent upon the action of secreted proteins. For example, Saxon *et al.*, *Biochem Soc Trans* 1997 May;25(2):383-7, discusses secreted IgE proteins.

For a further review of secreted proteins, see Nilsen-Hamilton *et al.*, *Cell Biol Int Rep* 1982 Sep;6(9):815-36.

Retinoic Acids and Retinoic Acid Receptors

Retinoids, or vitamin A metabolites/derivatives, have been determined to play essential roles in many aspects of development, metabolism and reproduction in vertebrates (see, for example, *The Retinoids*, Second Edition, Sporn *et al.* (Raven Press, New York, 1994)). There are two classes of retinoid receptors: the retinoic acid receptors (RARs), which bind to both all-trans retinoic acid (atRA) and 9-cis retinoic acid (9cRA), and the retinoid X receptors (RXRs), which bind only to 9cRA. These receptors modulate ligand-dependent gene expression by interacting as RXR/RAR heterodimers or RXR homodimers on specific target gene DNA sequences known as hormone response elements. In addition to their role in retinoid signalling, RXRs also serve as heterodimeric partners of nuclear receptors for vitamin D, thyroid hormone, and peroxisome proliferators (reviewed by Mangelsdorf *et al.*, at pages 319-349 of *The Retinoids*, Second Edition, Sporn *et al.* (Raven Press, New York, 1994)).

A number of studies have demonstrated that retinoids are essential for normal growth, vision, tissue homeostasis, reproduction and overall survival (for reviews and references, See Sporn *et al.*, *The Retinoids*, Vols. 1 and 2, Sporn *et al.*, eds., Academic Press, Orlando, Fla. (1984)). For example, retinoids have been shown to be vital to the maintenance of skin homeostasis and barrier function in mammals (Fisher, G. J., and

Voorhees, J. J., FASEB J. 10:1002-1013 (1996)). Retinoids are also apparently crucial during embryogenesis, since offspring of dams with vitamin A deficiency (VAD) exhibit a number of developmental defects (Wilson, J. G., et al., Am. J. Anat. 92:189-217 (1953); Morriss-Kay, G. M., and Sokolova, N., FASEB J. 10:961-968 (1996)). With the exceptions of those on vision (Wald, G., et al., Science 162:230-239 (1968)) and spermatogenesis in mammals (van Pelt, H. M. M., and De Rooij, D. G., Endocrinology 128:697-704 (1991)), most of the effects generated by VAD in animals and their fetuses can be prevented and/or reversed by retinoic acid (RA) administration (Wilson, J. G., et al., Am. J. Anat. 92:189-217 (1953); Thompson et al., Proc. Royal Soc. 159:510-535 (1964); Morriss-Kay, G. M., and Sokolova, N., FASEB J. 10:961-968 (1996)). The dramatic teratogenic effects of maternal RA administration on mammalian embryos (Shenefelt, R. E., Teratology 5, 103-108 (1972); Kessel, M., Development 115:487-501 (1992); Creech Kraft, J., In Retinoids in Normal Development and Teratogenesis, G. M. Morriss-Kay, ed., Oxford University Press, Oxford, UK, pp. 267-280 (1992)), and the marked effects of topical administration of retinoids on embryonic development of vertebrates and limb regeneration in amphibians (Mohanty-Hejmadi et al., Nature 355:352-353 (1992); Tabin, C. J., Cell 66:199-217 (1991)), have contributed to the notion that RA may have critical roles in morphogenesis and organogenesis.

Many synthetic structural analogues of all-trans retinoic acid or 9-cis-retinoic acid, commonly termed "retinoids", have been described in the literature to date. Some of these molecules are able to bind to, and specifically activate, the RARs or, on the other hand, the RXRs. Furthermore, some analogues are able to bind to, and activate a particular RAR receptor subtype (.alpha., .beta. or .gamma.). Finally, other analogues do not exhibit any particular selective activity with regard to these different receptors. In this respect, and by way of example, 9-cis-retinoic acid activates the RARs and the RXRs at one and the same time without any noteworthy selectivity for either of these receptors (nonspecific agonist ligand), whereas all-trans retinoic acid selectively activates the RARs (RAR-specific agonist ligand), with all subtypes being included. In a general manner, and qualitatively, a given substance (or ligand) is said to be specific for a given family of receptors (or, respectively, for a particular receptor of this family) when the said substance exhibits an affinity for all the receptors of this family (or, respectively, for

the particular receptor of this family) which is stronger than that which it otherwise exhibits for all the receptors of any other family (or, respectively, for all the other receptors, of this same family or not).

The genetic activities of the RA signal are mediated through the two families of receptors--the RAR family and the RXR family--which belong to the superfamily of ligand-inducible transcriptional regulatory factors that include steroid/thyroid hormone and vitamin D3 receptors (for reviews see Leid et al., *TIBS* 17:427-433 (1992); Chambon, P., *Semin. Cell Biol.* 5:115-125 (1994); Chambon, P., *FASEB J.* 10:940-954 (1996); Giguere, V., *Endocrinol. Rev.* 15:61-79 (1994); Mangelsdorf, D. J., and Evans, R. M., *Cell* 83:841-850 (1995); Gronemeyer, H., and Laudet, V., *Protein Profile* 2:1173-1236 (1995)).

RARs are the critical factors in tissue differentiation and development. They are up-regulated in rapidly dividing cells and tumors. RARs play an important role in lymphocyte activation. Synthetic antagonists of retinoic acid receptors can inhibit delayed type hypersensitivity (DTH). Growth factors and carotene regulate RXR expression levels. For example, granulocyte macrophage colony-stimulating factor induces retinoic acid receptors in myeloid leukemia cells.

Retinoic acid receptors can form heterodimers with other nuclear receptors. The protein provided by the present invention can be used as a probe to detect possible interactions in the two-hybrid assay. Synthetic peptides that mimic dimerization surface can disrupt intermolecular interactions between these receptors. RAR gene rearrangements are the primary causes of some types of leukemia and provide a convenient genetic marker for malignant cell lines. A number of retinoic acid derivatives are used in treatment of myelodysplastic disorders. They are designed to bind and activate RXRs. Beta-carotene can prevent skin tumor formation in mouse models. N-(4-hydroxyphenyl)retinamide can delay onset of dysplasia in bronchi. Different chemopreventive drugs can be designed to target individual retinoic receptors. The sequences provided by the present invention may be used to design high affinity chemopreventive compounds.

Although both the RARs and RXRs respond to all-trans-retinoic acid in vivo, the receptors differ in several important aspects. First, the RARs and RXRs are significantly

divergent in primary structure (e.g., the ligand binding domains of RAR.alpha. and RXR.alpha. have only 27% amino acid identity). These structural differences are reflected in the different relative degrees of responsiveness of RARs and RXRs to various vitamin A metabolites and synthetic retinoids. In addition, distinctly different patterns of tissue distribution are seen for RARs and RXRs. For example, in contrast to the RARs, which are generally not expressed at high levels in the visceral tissues, RXR.alpha. mRNA has been shown to be most abundant in the liver, kidney, lung, muscle and intestine. Finally, the RARs and RXRs have different target gene specificity. For example, response elements have recently been identified in the cellular retinal binding protein type II (CRBP II) and apolipoprotein AI genes which confer responsiveness to RXR, but not RAR. Furthermore, RAR has also been recently shown to repress RXR-mediated activation through the CRBP II RXR response element (Mangelsdorf et al., Cell, 66:555-61 (1991)). These data indicate that two retinoic acid responsive pathways are not simply redundant, but instead manifest a complex interplay. Recently, Heyman et al. (Cell, 68:397-406 (1992)) and Levin et al. (Nature, 355:359-61 (1992)) independently demonstrated that 9-cis-retinoic acid is a natural endogenous ligand for the RXRs. 9-cis-retinoic acid was shown to bind and transactivate the RXRs, as well as the RARs, and therefore appears to act as a "bifunctional" ligand.

RAR Receptors

Receptors belonging to the RAR family (RAR.alpha., .beta. and .gamma. and their isoforms) are activated by both all-trans- and 9-cis-RA (Leid et al., TIBS 17:427-433 (1992); Chambon, P., Semin. Cell Biol. 5:115-125 (1994); Dolle, P., et al., Mech. Dev. 45:91-104 (1994); Chambon, P., FASEB J. 10:940-954 (1996)). Within a given species, the DNA binding (C) and the ligand binding (E) domains of the three RAR types are highly similar, whereas the C-terminal domain F and the middle domain D exhibit no or little similarity. The amino acid sequences of the three RAR types are also notably different in their B regions, and their main isoforms (.alpha.1 and .alpha.2, .beta.1 to .beta.4, and .gamma.1 and .gamma.2) further differ in their N-terminal A regions (Leid et al., TIBS 17:427-433 (1992)). Amino acid sequence comparisons have revealed that the interspecies conservation of a given RAR type is greater than the similarity found between the three RAR types within a given species (Leid et al., TIBS 17:427-433

(1992)). This interspecies conservation is particularly striking in the N-terminal A regions of the various RAR.alpha., .beta. and .gamma. isoforms, whose A region amino acid sequences are quite divergent. Taken together with the distinct spatio-temporal expression patterns observed for the transcripts of each RAR and RXR type in the developing embryo and in various adult mouse tissues (Zelent, A., et al., *Nature* 339:714-717 (1989); Dolle, P., et al., *Nature* 342:702-705 (1989); Dolle et al., *Development* 110:1133-1151 (1990); Ruberte et al., *Development* 108:213-222 (1990); Ruberte et al., *Development* 111:45-60 (1991); Mangelsdorf et al., *Genes & Dev.* 6:329-344 (1992)), this interspecies conservation has suggested that each RAR type (and isoform) may perform unique functions. This hypothesis is further supported by the finding that the various RAR isoforms contain two transcriptional activation functions (AFs) located in the N-terminal A/B region (AF-1) and in the C-terminal E region (AF-2), which can synergistically, and to some extent differentially, activate various RA-responsive promoters (Leid et al., *TIBS* 17:427-433 (1992); Nagpal, S., et al., *Cell* 70:1007-1019 (1992); Nagpal, S., et al., *EMBO J.* 12:2349-2360 (1993)).

RXR Receptors

Unlike the RARs, members of the retinoid X receptor family (RXR.alpha., .beta. and .gamma.) are activated exclusively by 9-cis-RA (Chambon, P., *FASEB J.* 10:940-954 (1996); Chambon, P., *Semin. Cell Biol.* 5:115-125 (1994); Dolle, P., et al., *Mech. Dev.* 45:91-104 (1994); Linney, E., *Current Topics in Dev. Biol.* 27:309-350 (1992); Leid et al., *TIBS* 17:427-433 (1992); Kastner et al., in *Vitamin A in Health and Disease*, R. Blomhoff, ed., Marcel Dekker, New York (1993)). However, the RXRs characterized to date are similar to the RARs in that the different RXR types also differ markedly in their N-terminal A/B regions (Leid et al., *TIBS* 17:427-433 (1992); Leid et al., *Cell* 68:377-395 (1992); Mangelsdorf et al., *Genes and Dev.* 6:329-344 (1992)), and contain the same transcriptional activation functions in their N-terminal A/B region and C-terminal E region (Leid et al., *TIBS* 17:427-433 (1992); Nagpal, S., et al., *Cell* 70:1007-1019 (1992); Nagpal, S., et al., *EMBO J.* 12:2349-2360 (1993)).

RXR.alpha. and RXR.beta. have a widespread (possibly ubiquitous) expression pattern during mouse development and in the adult animal, being found in all fetal and adult tissues thus far examined (Mangelsdorf, D. J., et al., *Genes & Devel.* 6:329-344

(1992); Dolle, P., et al., *Mech. Devel.* 45:91-104 (1994); Nagata, T., et al., *Gene* 142:183-189 (1994)). RXR.gamma. transcripts, however, appear to have a more restricted distribution, being expressed in developing skeletal muscle in the embryo (where their expression persists throughout life), in the heart (after birth), in sensory epithelia of the visual and auditory systems, in specific structures of the central nervous system, and in tissues involved in thyroid hormone homeostasis, e.g., the thyroid gland and thyrotrope cells in the pituitary (Mangelsdorf, D. J., et al., *Genes & Devel.* 6:329-344 (1992); Dolle, P., et al., *Mech. Devel.* 45:91-104 (1994); Sugawara, A., et al., *Endocrinology* 136:1766-1774 (1995); Liu, Q., and Linney, E., *Mol. Endocrinol.* 7:651-658 (1993)).

It is currently unclear whether all the molecular properties of RXRs characterized in vitro are relevant for their physiological functions in vivo. In particular, it is unknown under what conditions these receptors act as 9-cis-RA-dependent transcriptional regulators (Chambon, P., *Semin. Cell Biol.* 5:115-125 (1994)). The knock-outs of RXR.alpha. and RXR.beta. in the mouse have provided some insight into the physiological functions of these receptors. For example, the ocular and cardiac malformations observed in RXR.alpha..sup.-/- fetuses (Kastner, P., et al., *Cell* 78:987-1003 (1994); Sucov, H. M., et al., *Genes & Devel.* 8:1007-1018 (1994)) are similar to those found in the fetal VAD syndrome, thus suggesting an important function of RXR.alpha. in the transduction of a retinoid signal during development. The involvement of RXRs in retinoid signaling is further supported by studies of compound RXR.alpha./RAR mutants, which reveal defects that are either absent or less severe in the single mutants (Kastner, P., et al., *Cell* 78:987-1003 (1994); Kastner, P., et al., *Cell* 83:859-869 (1995)). Interestingly, however, knockout of RXR.gamma. in the mouse induces no overt deleterious effects, and RXR.gamma..sup.-/- homozygotes which are also RXR.alpha..sup.-/- or RXR.beta..sup.-/- exhibit no additional abnormalities beyond those seen in RXR.alpha..sup.-/-, RXR.beta..sup.-/- and fetal VAD syndrome fetuses (Krezel, W., et al., *Proc. Natl. Acad. Sci. USA* 93(17):9010-9014 (1996)), suggesting that RXR.gamma., despite its highly tissue-specific expression pattern in the developing embryo, is dispensable for embryonic development and postnatal life in the mouse. The observation that live-born RXR.gamma..sup.-/- /RXR.beta..sup.-/- /RXR.alpha..sup.-/- mutants can grow to reach adult age (Krezel et al., *Proc. Natl. Acad. Sci. USA*

93(17):9010-9014 (1996)) indicates that a single RXR.alpha. allele is sufficient to carry out all of the vital developmental and postnatal functions of the RXR family of receptors, particularly all of the developmental functions which depend on RARs and may require RXR partnership (Dolle, P., et al., Mech. Dev. 45:91-104 (1994); Kastner, P., et al., Cell 83:859-869 (1995)). Furthermore, the finding that RXR.alpha..sup.-/- /RXR.gamma..sup.-/- double mutant embryos are not more affected than are single RXR.alpha..sup.-/- mutants (Krezel et al., Proc. Natl. Acad. Sci. USA 93(17):9010-9014 (1996)) clearly shows that RXR.beta. alone can also perform some of these functions. Therefore, the fact that RXR.alpha. alone and, to a certain extent RXR.beta. alone, are sufficient for the completion of a number of developmental RXR functions, clearly indicates the existence of a large degree of functional redundancy amongst RXRs. In this respect, the RXR situation is different from that of RARs, since all of types of RAR double mutants displayed much broader sets of defects than single mutants (Rowe, A., et al., Develop. 111:771-778 (1991); Lohnes, D., et al., Develop. 120:2723-2748 (1994); Mendelsohn, C., Develop. 120:2749-2771 (1994)).

Retinoid Binding to RAR and RXR Receptors

The crystal structures of the ligand-binding domains (LBDs) of the RARs and RXRs have recently been elucidated (Bourget, W., et al., Nature 375:377-382 (1995); Renaud, J. P., et al., Nature 378:681-689 (1995); Wurtz, J. M., et al., Nature Struct. Biol. 3:87-94 (1996)). Among the various RAR types, substantial amino acid sequence identity is observed in these domains: comparison of the LBDs of RAR.alpha., RAR.beta. and RAR.gamma. indicates that only three amino acid residues are variable in the ligand-binding pocket of these receptors. These residues apparently account for the fact that the various RAR types exhibit some selectivity in binding certain synthetic retinoids (Chen, J. -Y., et al., EMBO J. 14(6):1187-1197 (1995); Renaud, J. P., et al., Nature 378:681-689 (1995)), and consideration of these divergent residues can be used to design RAR type-specific synthetic retinoids which may be agonistic or antagonistic (Chambon, P., FASEB J. 10:940-954 (1996)). This design approach may be extendable generally to other nuclear receptors, such as thyroid receptor .alpha. (Wagner, R. L., et al., Nature 378:690-697 (1995)), the ligand-binding pockets of which may chemically and structurally resemble those of the RARs (Chambon, P., FASEB J. 10:940-954 (1996)). Conversely,

molecular modeling of the ligand-binding pocket of the RXRs demonstrates that there are no overt differences in amino acid composition between RXR.alpha., RXR.beta. and RXR.gamma. (Bourguet, W., et al., *Nature* 375:377-382 (1995); Wurtz, J. M., et al., *Nature Struct. Biol.* 3:87-94 (1996)), suggesting that design of type-specific synthetic ligands for the RXRs may be more difficult than for the RARs (Chambon, P., *FASEB J.* 10:940-954 (1996)).

Retinoid Signaling Through RAR:RXR Heterodimers

Nuclear receptors (NRs) are members of a superfamily of ligand-inducible transcriptional regulatory factors that include receptors for steroid hormones, thyroid hormones, vitamin D3 and retinoids (Leid, M., et al., *Trends Biochem. Sci.* 17:427-433 (1992); Leid, M., et al., *Cell* 68:377-395 (1992); and Linney, E. *Curr. Top. Dev. Biol.*, 27:309-350 (1992)). NRs exhibit a modular structure which reflects the existence of several autonomous functional domains. Based on amino acid sequence similarity between the chicken estrogen receptor, the human estrogen and glucocorticoid receptors, and the v-erb-A oncogene (Krust, A., et al., *EMBO J.* 5:891-897 (1986)), defined six regions--A, B, C, D, E and F--which display different degrees of evolutionary conservation amongst various members of the nuclear receptor superfamily. The highly conserved region C contains two zinc fingers and corresponds to the core of the DNA-binding domain (DBD), which is responsible for specific recognition of the cognate response elements. Region E is functionally complex, since in addition to the ligand-binding domain (LBD), it contains a ligand-dependent activation function (AF-2) and a dimerization interface. An autonomous transcriptional activation function (AF-1) is present in the non-conserved N-terminal A/B regions of the steroid receptors. Interestingly, both AF-1 and AF-2 of steroid receptors exhibit differential transcriptional activation properties which appear to be both cell type and promoter context specific (Gronemeyer, H. *Annu. Rev. Genet.* 25:89-123 (1991)).

As described above, the all-trans (T-RA) and 9-cis (9C-RA) retinoic acid signals are transduced by two families of nuclear receptors, RAR .alpha., .beta. and .gamma. (and their isoforms) are activated by both T-RA and 9C-RA, whereas RXR .alpha., .beta. and .gamma. are exclusively activated by 9C-RA (Allenby, G. et al., *Proc. Natl. Acad. Sci. USA* 90:30-34 (1993)). The three RAR types differ in their B regions, and their main

isoforms (.alpha.1 and .alpha.2, .beta.1-4, and .gamma.1 and .gamma.2) have different N-terminal A regions (Leid, M. et al., Trends Biochem. Sci. 17:427-433 (1992)). Similarly, the RXR types differ in their A/B regions (Mangelsdorf, D. J. et al., Genes Dev. 6:329-344 (1992)).

The E-region of RARs and RXRs has also been shown to contain a dimerization interface (Yu, V. C. et al., Curr. Opin. Biotechnol. 3:597-602 (1992)). Most interestingly, it was demonstrated that RAR/RXR heterodimers bind much more efficiently in vitro than homodimers of either receptor to a number of RA response elements (RAREs, also known as retinoic acid receptor responders) (Yu, V. C. et al., Cell 67:1251-1266 (1991); Berrodin, T. J. et al., Mol. Endocrinol 6:1468-1478 (1992); Bugge, T. H. et al., EMBO J. 11:1409-1418 (1992); Hall, R. K. et al., Mol. Cell. Biol. 12: 5527-5535 (1992); Hallenbeck P. L. et al., Proc. Natl. Acad. Sci. USA 89:5572-5576 (1992); Husmann, M. et al., Biochem. Biophys. Res. Commun. 187:1558-1564 (1992); Kliewer, S. A. et al., Nature 355:446-449 (1992); Leid, M. et al., Cell 68:377-395 (1992); Marks, M. S. et al., EMBO J. 11:1419-1435 (1992); Zhang, X. K. et al., Nature 355:441-446 (1992)). RAR and RXR heterodimers are also preferentially formed in solution in vitro (Yu, V. C. et al., Cell 67:1251-1266 (1991); Leid, M. et al., Cell 68:377-395 (1992); Marks, M. S. et al., EMBO J. 11:1419-1435 (1992)), although the addition of 9C-RA appears to enhance the formation of RXR homodimers in vitro (Lehman, J. M. et al., Science 258:1944-1946 (1992); Zhang, X. K. et al., Nature 358:587-591 (1992b)).

It has been shown that activation of RA-responsive promoters likely occurs through RAR:RXR heterodimers rather than through homodimers (Yu, V. C. et al., Cell 67:1251-1266 (1991); Leid et al., Cell 68:377-395 (1992b); Durand et al., Cell 71:73-85 (1992); Nagpal et al., Cell 70:1007-1019 (1992); Zhang, X. K., et al., Nature 355, 441-446 (1992); Kliewer et al., Nature 355:446-449 (1992); Bugge et al., EMBO J. 11: 1409-1418 (1992); Marks et al., EMBO J. 11:1419-1435 (1992); Yu, V. C. et al., Cur. Op. Biotech. 3:597-602 (1992); Leid et al., TIBS 17:427-433 (1992); Laudet and Stehelin, Curr. Biol. 2:293-295 (1992); Green, S., Nature 361:590-591 (1993)). The RXR portion of these heterodimers has been proposed to be silent in retinoid-induced signaling (Kurokawa, R., et al., Nature 371:528-531 (1994); Forman, B. M., et al., Cell 81:541-550 (1995); Mangelsdorf, D. J., and Evans, R. M., Cell 83:835-850 (1995)), although

conflicting results have been reported on this issue (Apfel, C. M., et al., J. Biol. Chem. 270(51):30765-30772 (1995); see Chambon, P., FASEB J. 10:940-954 (1996) for review). Although the results of these studies strongly suggest that RAR/RXR heterodimers are indeed functional units that transduce the RA signal in vivo, it is unclear whether all of the suggested heterodimeric combinations occur in vivo (Chambon, P., Semin. Cell Biol. 5:115-125 (1994)). Thus, the basis for the highly pleiotropic effect of retinoids may reside, at least in part, in the control of different subsets of retinoid-responsive promoters by cell-specifically expressed heterodimeric combinations of RAR:RXR types (and isoforms), whose activity may be in turn regulated by cell-specific levels of all-trans- and 9-cis-RA (Leid et al., TIBS 17:427-433 (1992)).

The RXR receptors may also be involved in RA-independent signaling. For example, the observation of aberrant lipid metabolism in the Sertoli cells of RXR.beta..sup.-/- mutant animals suggests that functional interactions may also occur between RXR.beta. and the peroxisomal proliferator-activated receptor signaling pathway (WO 94/26100; Kastner, P., et al., Genes & Devel. 10:80-92 (1996)).

For a further review of retinoic acid receptors, see: Shimizu et al., Cancer Res 2000 Aug 15;60(16):4544-9; Ponnamperna et al., Nutr Cancer 2000;37(1):82-8; Yoshimura et al., J Med Chem 2000 Jul 27;43(15):2929-37; Kurie et al., Clin Cancer Res 2000 Aug;6(8):2973-9; Lee et al., J Biol Chem 2000 Aug 17; and Sainty et al., Blood 2000 Aug 15;96(4):1287-96.

Secreted proteins, particularly members of the retinoic acid receptor responder secreted protein subfamily, are a major target for drug action and development. Accordingly, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown members of this subfamily of secreted proteins. The present invention advances the state of the art by providing previously unidentified human secreted proteins that have homology to members of the retinoic acid receptor responder secreted protein subfamily.

SUMMARY OF THE INVENTION

The present invention is based in part on the identification of amino acid sequences of human secreted peptides and proteins that are related to the retinoic acid

receptor responder secreted protein subfamily, as well as allelic variants and other mammalian orthologs thereof. These unique peptide sequences, and nucleic acid sequences that encode these peptides, can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate secreted protein activity in cells and tissues that express the secreted protein.

DESCRIPTION OF THE FIGURE SHEETS

FIGURE 1 provides the nucleotide sequence of a cDNA molecule or transcript sequence that encodes the secreted protein of the present invention. (SEQ ID NO:1) In addition, structure and functional information is provided, such as ATG start, stop and tissue distribution, where available, that allows one to readily determine specific uses of inventions based on this molecular sequence.

FIGURE 2 provides the predicted amino acid sequence of the secreted protein of the present invention. (SEQ ID NO:2) In addition structure and functional information such as protein family, function, and modification sites is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence.

FIGURE 3 provides genomic sequences that span the gene encoding the secreted protein of the present invention. (SEQ ID NO:3) In addition structure and functional information, such as intron/exon structure, promoter location, etc., is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence. As indicated by the data presented in Figure 3, the map position was determined to be on chromosome 16.

DETAILED DESCRIPTION OF THE INVENTION

General Description

The present invention is based on the sequencing of the human genome. During the sequencing and assembly of the human genome, analysis of the sequence information

revealed previously unidentified fragments of the human genome that encode peptides that share structural and/or sequence homology to protein/peptide/domains identified and characterized within the art as being a secreted protein or part of a secreted protein and are related to the retinoic acid receptor responder secreted protein subfamily. Utilizing these sequences, additional genomic sequences were assembled and transcript and/or cDNA sequences were isolated and characterized. Based on this analysis, the present invention provides amino acid sequences of human secreted peptides and proteins that are related to the retinoic acid receptor responder secreted protein subfamily, nucleic acid sequences in the form of transcript sequences, cDNA sequences and/or genomic sequences that encode these secreted peptides and proteins, nucleic acid variation (allelic information), tissue distribution of expression, and information about the closest art known protein/peptide/domain that has structural or sequence homology to the secreted protein of the present invention.

In addition to being previously unknown, the peptides that are provided in the present invention are selected based on their ability to be used for the development of commercially important products and services. Specifically, the present peptides are selected based on homology and/or structural relatedness to known secreted proteins of the retinoic acid receptor responder secreted protein subfamily and the expression pattern observed. The art has clearly established the commercial importance of members of this family of proteins and proteins that have expression patterns similar to that of the present gene. Some of the more specific features of the peptides of the present invention, and the uses thereof, are described herein, particularly in the Background of the Invention and in the annotation provided in the Figures, and/or are known within the art for each of the known retinoic acid receptor responder family or subfamily of secreted proteins.

Specific Embodiments

Peptide Molecules

The present invention provides nucleic acid sequences that encode protein molecules that have been identified as being members of the secreted protein family of proteins and are related to the retinoic acid receptor responder secreted protein subfamily

(protein sequences are provided in Figure 2, transcript/cDNA sequences are provided in Figure 1 and genomic sequences are provided in Figure 3). The peptide sequences provided in Figure 2, as well as the obvious variants described herein, particularly allelic variants as identified herein and using the information in Figure 3, will be referred herein as the secreted peptides of the present invention, secreted peptides, or peptides/proteins of the present invention.

The present invention provides isolated peptide and protein molecules that consist of, consist essentially of, or comprise the amino acid sequences of the secreted peptides disclosed in the Figure 2, (encoded by the nucleic acid molecule shown in Figure 1, transcript/cDNA or Figure 3, genomic sequence), as well as all obvious variants of these peptides that are within the art to make and use. Some of these variants are described in detail below.

As used herein, a peptide is said to be "isolated" or "purified" when it is substantially free of cellular material or free of chemical precursors or other chemicals. The peptides of the present invention can be purified to homogeneity or other degrees of purity. The level of purification will be based on the intended use. The critical feature is that the preparation allows for the desired function of the peptide, even if in the presence of considerable amounts of other components (the features of an isolated nucleic acid molecule is discussed below).

In some uses, "substantially free of cellular material" includes preparations of the peptide having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins. When the peptide is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of the peptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the secreted peptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less

than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

The isolated secreted peptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. For example, a nucleic acid molecule encoding the secreted peptide is cloned into an expression vector, the expression vector introduced into a host cell and the protein expressed in the host cell. The protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Many of these techniques are described in detail below.

Accordingly, the present invention provides proteins that consist of the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). The amino acid sequence of such a protein is provided in Figure 2. A protein consists of an amino acid sequence when the amino acid sequence is the final amino acid sequence of the protein.

The present invention further provides proteins that consist essentially of the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). A protein consists essentially of an amino acid sequence when such an amino acid sequence is present with only a few additional amino acid residues, for example from about 1 to about 100 or so additional residues, typically from 1 to about 20 additional residues in the final protein.

The present invention further provides proteins that comprise the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). A protein comprises an amino acid sequence when the amino acid sequence is at least part of the final amino acid sequence of the protein. In such a fashion, the protein can be only the peptide or have additional amino acid molecules, such as amino acid residues (contiguous encoded sequence) that are naturally associated with it or heterologous amino acid residues/peptide sequences. Such a protein can have a few additional amino acid residues or can comprise several hundred or

more additional amino acids. The preferred classes of proteins that are comprised of the secreted peptides of the present invention are the naturally occurring mature proteins. A brief description of how various types of these proteins can be made/isolated is provided below.

The secreted peptides of the present invention can be attached to heterologous sequences to form chimeric or fusion proteins. Such chimeric and fusion proteins comprise a secreted peptide operatively linked to a heterologous protein having an amino acid sequence not substantially homologous to the secreted peptide. "Operatively linked" indicates that the secreted peptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the secreted peptide.

In some uses, the fusion protein does not affect the activity of the secreted peptide *per se*. For example, the fusion protein can include, but is not limited to, enzymatic fusion proteins, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions, MYC-tagged, HI-tagged and Ig fusions. Such fusion proteins, particularly poly-His fusions, can facilitate the purification of recombinant secreted peptide. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a protein can be increased by using a heterologous signal sequence.

A chimeric or fusion protein can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different protein sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A secreted peptide-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the secreted peptide.

As mentioned above, the present invention also provides and enables obvious variants of the amino acid sequence of the proteins of the present invention, such as

naturally occurring mature forms of the peptide, allelic/sequence variants of the peptides, non-naturally occurring recombinantly derived variants of the peptides, and orthologs and paralogs of the peptides. Such variants can readily be generated using art-known techniques in the fields of recombinant nucleic acid technology and protein biochemistry. It is understood, however, that variants exclude any amino acid sequences disclosed prior to the invention.

Such variants can readily be identified/made using molecular techniques and the sequence information disclosed herein. Further, such variants can readily be distinguished from other peptides based on sequence and/or structural homology to the secreted peptides of the present invention. The degree of homology/identity present will be based primarily on whether the peptide is a functional variant or non-functional variant, the amount of divergence present in the paralog family and the evolutionary distance between the orthologs.

To determine the percent identity of two amino acid sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% or more of the length of a reference sequence is aligned for comparison purposes. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm.

(*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York,

1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)) (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

Full-length pre-processed forms, as well as mature processed forms, of proteins that comprise one of the peptides of the present invention can readily be identified as having complete sequence identity to one of the secreted peptides of the present invention as well as being encoded by the same genetic locus as the secreted peptide provided herein.

Allelic variants of a secreted peptide can readily be identified as being a human protein having a high degree (significant) of sequence homology/identity to at least a portion of the secreted peptide as well as being encoded by the same genetic locus as the secreted peptide provided herein. Genetic locus can readily be determined based on the genomic information provided in Figure 3, such as the genomic sequence mapped to the reference human. As indicated by the data presented in Figure 3, the map position was determined to be on chromosome 16. As used herein, two proteins (or a region of the proteins) have significant homology when the amino acid sequences are typically at least about 70-80%, 80-90%, and more typically at least about 90-95% or more homologous. A significantly homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid sequence that will hybridize to a secreted peptide encoding nucleic acid molecule under stringent conditions as more fully described below.

Figure 3 provides SNP information that has been found in a gene encoding the transporter proteins of the present invention. The following variations were identified: T948-, G1149A, G4199C, T4352G, A6493G, T14047GA, G14136T, G14238A, T14260G, C25736T, G26321A, A31359G, T35098G, C40532G, A41706G, G51095C, G53101C, G54556C, - 61872T, G62172C, A62860C, C67086A, A67621C, A70582T, C74175-, T74478C, T77092G, T77328C, G77385A, C77947T, G79395C, -81111C, and G81610A.

Paralogs of a secreted peptide can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the secreted peptide, as being encoded by a gene from humans, and as having similar activity or function. Two proteins will typically be considered paralogs when the amino acid sequences are typically at least about 60% or greater, and more typically at least about 70% or greater homology through a given region or domain. Such paralogs will be encoded by a nucleic acid sequence that will hybridize to a secreted peptide encoding nucleic acid molecule under moderate to stringent conditions as more fully described below.

Orthologs of a secreted peptide can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the secreted peptide as well as being encoded by a gene from another organism. Preferred orthologs will be isolated from mammals, preferably primates, for the development of human therapeutic targets and agents. Such orthologs will be encoded by a nucleic acid sequence that will hybridize to a secreted peptide encoding nucleic acid molecule under moderate to stringent conditions, as more fully described below, depending on the degree of relatedness of the two organisms yielding the proteins.

Non-naturally occurring variants of the secreted peptides of the present invention can readily be generated using recombinant techniques. Such variants include, but are not limited to deletions, additions and substitutions in the amino acid sequence of the secreted peptide. For example, one class of substitutions are conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a secreted peptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile; interchange of the hydroxyl residues Ser and Thr; exchange of the acidic residues Asp and Glu; substitution between the amide residues Asn and Gln; exchange of the basic residues Lys and Arg; and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

Variant secreted peptides can be fully functional or can lack function in one or more activities, e.g. ability to bind substrate, ability to phosphorylate substrate, ability to mediate signaling, etc. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Figure 2 provides the result of protein analysis and can be used to identify critical domains/regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree.

Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)), particularly using the results provided in Figure 2. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as secreted protein activity or in assays such as an *in vitro* proliferative activity. Sites that are critical for binding partner/substrate binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.* *Science* 255:306-312 (1992)).

The present invention further provides fragments of the secreted peptides, in addition to proteins and peptides that comprise and consist of such fragments, particularly those comprising the residues identified in Figure 2. The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that may be disclosed publicly prior to the present invention.

As used herein, a fragment comprises at least 8, 10, 12, 14, 16, or more contiguous amino acid residues from a secreted peptide. Such fragments can be chosen based on the ability to retain one or more of the biological activities of the secreted peptide or could be chosen for the ability to perform a function, e.g. bind a substrate or act as an immunogen. Particularly important fragments are biologically active fragments, peptides that are, for example, about 8 or more amino acids in length. Such fragments will typically comprise a domain or motif of the secreted peptide, e.g., active site or a substrate-binding domain. Further, possible fragments include, but are not limited to, domain or motif containing fragments, soluble peptide fragments, and fragments containing immunogenic structures. Predicted domains and functional sites are readily identifiable by computer programs well known and readily available to those of skill in the art (e.g., PROSITE analysis). The results of one such analysis are provided in Figure 2.

Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids. Further, many amino acids, including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Common modifications that occur naturally in secreted peptides are described in

basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art (some of these features are identified in Figure 2).

Known modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such modifications are well known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins - Structure and Molecular Properties*, 2nd Ed., T.E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as by Wold, F., *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York 1-12 (1983); Seifter *et al.* (*Meth. Enzymol.* 182: 626-646 (1990)) and Rattan *et al.* (*Ann. N.Y. Acad. Sci.* 663:48-62 (1992)).

Accordingly, the secreted peptides of the present invention also encompass derivatives or analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature secreted peptide is fused with another compound, such as a compound to increase the half-life of the secreted peptide (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature secreted peptide, such as a leader or secretory sequence or a sequence for purification of the mature secreted peptide or a pro-protein sequence.

Protein/Peptide Uses

The proteins of the present invention can be used in substantial and specific assays related to the functional information provided in the Figures; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; and as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state). Where the protein binds or potentially binds to another protein or ligand (such as, for example, in a secreted protein-effector protein interaction or secreted protein-ligand interaction), the protein can be used to identify the binding partner/ligand so as to develop a system to identify inhibitors of the binding interaction. Any or all of these uses are capable of being developed into reagent grade or kit format for commercialization as commercial products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

The potential uses of the peptides of the present invention are based primarily on the source of the protein as well as the class/action of the protein. For example, secreted proteins isolated from humans and their human/mammalian orthologs serve as targets for identifying agents for use in mammalian therapeutic applications, e.g. a human drug, particularly in modulating a biological or pathological response in a cell or tissue that expresses the secreted protein. A large percentage of pharmaceutical agents are being developed that modulate the activity of secreted proteins, particularly members of the retinoic acid receptor responder subfamily (see Background of the Invention). The structural and functional information provided in the Background and Figures provide specific and substantial uses for the molecules of the present invention, particularly in combination with the expression information provided in Figure 1. Such uses can readily be determined using the information provided herein, that which is known in the art, and routine experimentation.

The proteins of the present invention (including variants and fragments that may have been disclosed prior to the present invention) are useful for biological assays related to secreted proteins that are related to members of the retinoic acid receptor responder subfamily. Such assays involve any of the known secreted protein functions or activities or properties useful for diagnosis and treatment of secreted protein-related conditions that are specific for the subfamily of secreted proteins that the one of the present invention belongs to, particularly in cells and tissues that express the secreted protein.

The proteins of the present invention are also useful in drug screening assays, in cell-based or cell-free systems. Cell-based systems can be native, i.e., cells that normally express the secreted protein, as a biopsy or expanded in cell culture. In an alternate embodiment, cell-based assays involve recombinant host cells expressing the secreted protein.

The polypeptides can be used to identify compounds that modulate secreted protein activity of the protein in its natural state or an altered form that causes a specific disease or pathology associated with the secreted protein. Both the secreted proteins of the present invention and appropriate variants and fragments can be used in high-throughput screens to assay candidate compounds for the ability to bind to the secreted protein. These compounds can be further screened against a functional secreted protein to determine the effect of the compound on the secreted protein activity. Further, these compounds can be tested in animal or invertebrate systems to determine activity/effectiveness. Compounds can be identified that activate (agonist) or inactivate (antagonist) the secreted protein to a desired degree.

Further, the proteins of the present invention can be used to screen a compound for the ability to stimulate or inhibit interaction between the secreted protein and a molecule that normally interacts with the secreted protein, e.g. a substrate or a component of the signal pathway that the secreted protein normally interacts (for example, another secreted protein). Such assays typically include the steps of combining the secreted protein with a candidate compound under conditions that allow the secreted protein, or fragment, to interact with the target molecule, and to detect the formation of a complex between the protein and the target or to detect the biochemical consequence of the interaction with the secreted protein and the target.

Candidate compounds include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.*, *Nature* 354:82-84 (1991); Houghten *et al.*, *Nature* 354:84-86 (1991)) and combinatorial chemistry-derived molecular libraries made of D- and/or L- configuration amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.*, *Cell* 72:767-778 (1993)); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')₂, Fab expression library fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules (e.g., molecules obtained from combinatorial and natural product libraries).

One candidate compound is a soluble fragment of the receptor that competes for substrate binding. Other candidate compounds include mutant secreted proteins or appropriate fragments containing mutations that affect secreted protein function and thus compete for substrate. Accordingly, a fragment that competes for substrate, for example with a higher affinity, or a fragment that binds substrate but does not allow release, is encompassed by the invention.

Any of the biological or biochemical functions mediated by the secreted protein can be used as an endpoint assay. These include all of the biochemical or biochemical/biological events described herein, in the references cited herein, incorporated by reference for these endpoint assay targets, and other functions known to those of ordinary skill in the art or that can be readily identified using the information provided in the Figures, particularly Figure 2. Specifically, a biological function of a cell or tissues that expresses the secreted protein can be assayed.

Binding and/or activating compounds can also be screened by using chimeric secreted proteins in which the amino terminal extracellular domain, or parts thereof, the entire transmembrane domain or subregions, such as any of the seven transmembrane segments or any of the intracellular or extracellular loops and the carboxy terminal intracellular domain, or parts thereof, can be replaced by heterologous domains or subregions. For example, a substrate-binding region can be used that interacts with a different substrate than that which is recognized by the native secreted protein. Accordingly, a different set of signal transduction components is available as an end-point

assay for activation. This allows for assays to be performed in other than the specific host cell from which the secreted protein is derived.

The proteins of the present invention are also useful in competition binding assays in methods designed to discover compounds that interact with the secreted protein (e.g. binding partners and/or ligands). Thus, a compound is exposed to a secreted protein polypeptide under conditions that allow the compound to bind or to otherwise interact with the polypeptide. Soluble secreted protein polypeptide is also added to the mixture. If the test compound interacts with the soluble secreted protein polypeptide, it decreases the amount of complex formed or activity from the secreted protein target. This type of assay is particularly useful in cases in which compounds are sought that interact with specific regions of the secreted protein. Thus, the soluble polypeptide that competes with the target secreted protein region is designed to contain peptide sequences corresponding to the region of interest.

To perform cell free drug screening assays, it is sometimes desirable to immobilize either the secreted protein, or fragment, or its target molecule to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay.

Techniques for immobilizing proteins on matrices can be used in the drug screening assays. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates (e.g., ^{35}S -labeled) and the candidate compound, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel determined directly, or in the supernatant after the complexes are dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of secreted protein-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques. For example, either the polypeptide or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin using techniques well known in the art. Alternatively, antibodies

reactive with the protein but which do not interfere with binding of the protein to its target molecule can be derivatized to the wells of the plate, and the protein trapped in the wells by antibody conjugation. Preparations of a secreted protein-binding protein and a candidate compound are incubated in the secreted protein-presenting wells and the amount of complex trapped in the well can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the secreted protein target molecule, or which are reactive with secreted protein and compete with the target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the target molecule.

Agents that modulate one of the secreted proteins of the present invention can be identified using one or more of the above assays, alone or in combination. It is generally preferable to use a cell-based or cell free system first and then confirm activity in an animal or other model system. Such model systems are well known in the art and can readily be employed in this context.

Modulators of secreted protein activity identified according to these drug screening assays can be used to treat a subject with a disorder mediated by the secreted protein pathway, by treating cells or tissues that express the secreted protein. These methods of treatment include the steps of administering a modulator of secreted protein activity in a pharmaceutical composition to a subject in need of such treatment, the modulator being identified as described herein.

In yet another aspect of the invention, the secreted proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins, which bind to or interact with the secreted protein and are involved in secreted protein activity.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for a secreted protein is fused to a gene encoding the DNA binding domain of a known

transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a secreted protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the secreted protein.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., a secreted protein-modulating agent, an antisense secreted protein nucleic acid molecule, a secreted protein-specific antibody, or a secreted protein-binding partner) can be used in an animal or other model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal or other model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

The secreted proteins of the present invention are also useful to provide a target for diagnosing a disease or predisposition to disease mediated by the peptide. Accordingly, the invention provides methods for detecting the presence, or levels of, the protein (or encoding mRNA) in a cell, tissue, or organism. The method involves contacting a biological sample with a compound capable of interacting with the secreted protein such that the interaction can be detected. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

One agent for detecting a protein in a sample is an antibody capable of selectively binding to protein. A biological sample includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject.

The peptides of the present invention also provide targets for diagnosing active protein activity, disease, or predisposition to disease, in a patient having a variant peptide, particularly activities and conditions that are known for other members of the family of proteins to which the present one belongs. Thus, the peptide can be isolated from a biological sample and assayed for the presence of a genetic mutation that results in aberrant peptide. This includes amino acid substitution, deletion, insertion, rearrangement, (as the result of aberrant splicing events), and inappropriate post-translational modification. Analytic methods include altered electrophoretic mobility, altered tryptic peptide digest, altered secreted protein activity in cell-based or cell-free assay, alteration in substrate or antibody-binding pattern, altered isoelectric point, direct amino acid sequencing, and any other of the known assay techniques useful for detecting mutations in a protein. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

In vitro techniques for detection of peptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence using a detection reagent, such as an antibody or protein binding agent. Alternatively, the peptide can be detected *in vivo* in a subject by introducing into the subject a labeled anti-peptide antibody or other types of detection agent. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques. Particularly useful are methods that detect the allelic variant of a peptide expressed in a subject and methods which detect fragments of a peptide in a sample.

The peptides are also useful in pharmacogenomic analysis. Pharmacogenomics deal with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Eichelbaum, M. (*Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985 (1996)), and Linder, M.W. (*Clin. Chem.* 43(2):254-266 (1997)). The clinical outcomes of these variations result in severe toxicity of therapeutic drugs in certain individuals or therapeutic failure of drugs in certain individuals as a result of individual variation in metabolism. Thus, the genotype of the individual can determine the way a therapeutic compound acts on the body or the way the body metabolizes the compound. Further, the activity of drug metabolizing enzymes effects both the intensity and duration of drug action. Thus, the pharmacogenomics of the individual

permit the selection of effective compounds and effective dosages of such compounds for prophylactic or therapeutic treatment based on the individual's genotype. The discovery of genetic polymorphisms in some drug metabolizing enzymes has explained why some patients do not obtain the expected drug effects, show an exaggerated drug effect, or experience serious toxicity from standard drug dosages. Polymorphisms can be expressed in the phenotype of the extensive metabolizer and the phenotype of the poor metabolizer. Accordingly, genetic polymorphism may lead to allelic protein variants of the secreted protein in which one or more of the secreted protein functions in one population is different from those in another population. The peptides thus allow a target to ascertain a genetic predisposition that can affect treatment modality. Thus, in a ligand-based treatment, polymorphism may give rise to amino terminal extracellular domains and/or other substrate-binding regions that are more or less active in substrate binding, and secreted protein activation. Accordingly, substrate dosage would necessarily be modified to maximize the therapeutic effect within a given population containing a polymorphism. As an alternative to genotyping, specific polymorphic peptides could be identified.

The peptides are also useful for treating a disorder characterized by an absence of, inappropriate, or unwanted expression of the protein. Accordingly, methods for treatment include the use of the secreted protein or fragments.

Antibodies

The invention also provides antibodies that selectively bind to one of the peptides of the present invention, a protein comprising such a peptide, as well as variants and fragments thereof. As used herein, an antibody selectively binds a target peptide when it binds the target peptide and does not significantly bind to unrelated proteins. An antibody is still considered to selectively bind a peptide even if it also binds to other proteins that are not substantially homologous with the target peptide so long as such proteins share homology with a fragment or domain of the peptide target of the antibody. In this case, it would be understood that antibody binding to the peptide is still selective despite some degree of cross-reactivity.

As used herein, an antibody is defined in terms consistent with that recognized within the art: they are multi-subunit proteins produced by a mammalian organism in

response to an antigen challenge. The antibodies of the present invention include polyclonal antibodies and monoclonal antibodies, as well as fragments of such antibodies, including, but not limited to, Fab or F(ab')₂, and Fv fragments.

Many methods are known for generating and/or identifying antibodies to a given target peptide. Several such methods are described by Harlow, *Antibodies*, Cold Spring Harbor Press, (1989).

In general, to generate antibodies, an isolated peptide is used as an immunogen and is administered to a mammalian organism, such as a rat, rabbit or mouse. The full-length protein, an antigenic peptide fragment or a fusion protein can be used. Particularly important fragments are those covering functional domains, such as the domains identified in Figure 2, and domain of sequence homology or divergence amongst the family, such as those that can readily be identified using protein alignment methods and as presented in the Figures.

Antibodies are preferably prepared from regions or discrete fragments of the secreted proteins. Antibodies can be prepared from any region of the peptide as described herein. However, preferred regions will include those involved in function/activity and/or secreted protein/binding partner interaction. Figure 2 can be used to identify particularly important regions while sequence alignment can be used to identify conserved and unique sequence fragments.

An antigenic fragment will typically comprise at least 8 contiguous amino acid residues. The antigenic peptide can comprise, however, at least 10, 12, 14, 16 or more amino acid residues. Such fragments can be selected on a physical property, such as fragments correspond to regions that are located on the surface of the protein, e.g., hydrophilic regions or can be selected based on sequence uniqueness (see Figure 2).

Detection on an antibody of the present invention can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include

umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Antibody Uses

The antibodies can be used to isolate one of the proteins of the present invention by standard techniques, such as affinity chromatography or immunoprecipitation. The antibodies can facilitate the purification of the natural protein from cells and recombinantly produced protein expressed in host cells. In addition, such antibodies are useful to detect the presence of one of the proteins of the present invention in cells or tissues to determine the pattern of expression of the protein among various tissues in an organism and over the course of normal development. Further, such antibodies can be used to detect protein *in situ*, *in vitro*, or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression. Also, such antibodies can be used to assess abnormal tissue distribution or abnormal expression during development or progression of a biological condition. Antibody detection of circulating fragments of the full length protein can be used to identify turnover.

Further, the antibodies can be used to assess expression in disease states such as in active stages of the disease or in an individual with a predisposition toward disease related to the protein's function. When a disorder is caused by an inappropriate tissue distribution, developmental expression, level of expression of the protein, or expressed/processed form, the antibody can be prepared against the normal protein. If a disorder is characterized by a specific mutation in the protein, antibodies specific for this mutant protein can be used to assay for the presence of the specific mutant protein.

The antibodies can also be used to assess normal and aberrant subcellular localization of cells in the various tissues in an organism. The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at correcting expression level or the presence of aberrant sequence and aberrant tissue distribution or developmental expression,

antibodies directed against the protein or relevant fragments can be used to monitor therapeutic efficacy.

Additionally, antibodies are useful in pharmacogenomic analysis. Thus, antibodies prepared against polymorphic proteins can be used to identify individuals that require modified treatment modalities. The antibodies are also useful as diagnostic tools as an immunological marker for aberrant protein analyzed by electrophoretic mobility, isoelectric point, tryptic peptide digest, and other physical assays known to those in the art.

The antibodies are also useful for tissue typing. Thus, where a specific protein has been correlated with expression in a specific tissue, antibodies that are specific for this protein can be used to identify a tissue type.

The antibodies are also useful for inhibiting protein function, for example, blocking the binding of the secreted peptide to a binding partner such as a substrate. These uses can also be applied in a therapeutic context in which treatment involves inhibiting the protein's function. An antibody can be used, for example, to block binding, thus modulating (agonizing or antagonizing) the peptides activity. Antibodies can be prepared against specific fragments containing sites required for function or against intact protein that is associated with a cell or cell membrane. See Figure 2 for structural information relating to the proteins of the present invention.

The invention also encompasses kits for using antibodies to detect the presence of a protein in a biological sample. The kit can comprise antibodies such as a labeled or labelable antibody and a compound or agent for detecting protein in a biological sample; means for determining the amount of protein in the sample; means for comparing the amount of protein in the sample with a standard; and instructions for use. Such a kit can be supplied to detect a single protein or epitope or can be configured to detect one of a multitude of epitopes, such as in an antibody detection array. Arrays are described in detail below for nucleic acid arrays and similar methods have been developed for antibody arrays.

Nucleic Acid Molecules

The present invention further provides isolated nucleic acid molecules that encode a secreted peptide or protein of the present invention (cDNA, transcript and genomic

sequence). Such nucleic acid molecules will consist of, consist essentially of, or comprise a nucleotide sequence that encodes one of the secreted peptides of the present invention, an allelic variant thereof, or an ortholog or paralog thereof.

As used herein, an "isolated" nucleic acid molecule is one that is separated from other nucleic acid present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. However, there can be some flanking nucleotide sequences, for example up to about 5KB, 4KB, 3KB, 2KB, or 1KB or less, particularly contiguous peptide encoding sequences and peptide encoding sequences within the same gene but separated by introns in the genomic sequence. The important point is that the nucleic acid is isolated from remote and unimportant flanking sequences such that it can be subjected to the specific manipulations described herein such as recombinant expression, preparation of probes and primers, and other uses specific to the nucleic acid sequences.

Moreover, an "isolated" nucleic acid molecule, such as a transcript/cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. However, the nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated.

For example, recombinant DNA molecules contained in a vector are considered isolated. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the isolated DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Accordingly, the present invention provides nucleic acid molecules that consist of the nucleotide sequence shown in Figure 1 or 3 (SEQ ID NO:1, transcript sequence and SEQ ID NO:3, genomic sequence), or any nucleic acid molecule that encodes the protein provided in Figure 2, SEQ ID NO:2. A nucleic acid molecule consists of a nucleotide sequence when the nucleotide sequence is the complete nucleotide sequence of the nucleic acid molecule.

The present invention further provides nucleic acid molecules that consist essentially of the nucleotide sequence shown in Figure 1 or 3 (SEQ ID NO:1, transcript sequence and SEQ ID NO:3, genomic sequence), or any nucleic acid molecule that encodes the protein provided in Figure 2, SEQ ID NO:2. A nucleic acid molecule consists essentially of a nucleotide sequence when such a nucleotide sequence is present with only a few additional nucleic acid residues in the final nucleic acid molecule.

The present invention further provides nucleic acid molecules that comprise the nucleotide sequences shown in Figure 1 or 3 (SEQ ID NO:1, transcript sequence and SEQ ID NO:3, genomic sequence), or any nucleic acid molecule that encodes the protein provided in Figure 2, SEQ ID NO:2. A nucleic acid molecule comprises a nucleotide sequence when the nucleotide sequence is at least part of the final nucleotide sequence of the nucleic acid molecule. In such a fashion, the nucleic acid molecule can be only the nucleotide sequence or have additional nucleic acid residues, such as nucleic acid residues that are naturally associated with it or heterologous nucleotide sequences. Such a nucleic acid molecule can have a few additional nucleotides or can comprises several hundred or more additional nucleotides. A brief description of how various types of these nucleic acid molecules can be readily made/isolated is provided below.

In Figures 1 and 3, both coding and non-coding sequences are provided. Because of the source of the present invention, humans genomic sequence (Figure 3) and cDNA/transcript sequences (Figure 1), the nucleic acid molecules in the Figures will contain genomic intronic sequences, 5' and 3' non-coding sequences, gene regulatory regions and non-coding intergenic sequences. In general such sequence features are either noted in Figures 1 and 3 or can readily be identified using computational tools known in the art. As discussed below, some of the non-coding regions, particularly gene regulatory elements such as promoters, are useful for a variety of purposes, e.g. control of heterologous gene expression, target for identifying gene activity modulating compounds, and are particularly claimed as fragments of the genomic sequence provided herein.

The isolated nucleic acid molecules can encode the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature peptide (when the mature form has more than one peptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, facilitate protein trafficking,

prolong or shorten protein half-life or facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in situ*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

As mentioned above, the isolated nucleic acid molecules include, but are not limited to, the sequence encoding the secreted peptide alone, the sequence encoding the mature peptide and additional coding sequences, such as a leader or secretory sequence (e.g., a pre-pro or pro-protein sequence), the sequence encoding the mature peptide, with or without the additional coding sequences, plus additional non-coding sequences, for example introns and non-coding 5' and 3' sequences such as transcribed but non-translated sequences that play a role in transcription, mRNA processing (including splicing and polyadenylation signals), ribosome binding and stability of mRNA. In addition, the nucleic acid molecule may be fused to a marker sequence encoding, for example, a peptide that facilitates purification.

Isolated nucleic acid molecules can be in the form of RNA, such as mRNA, or in the form DNA, including cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The nucleic acid, especially DNA, can be double-stranded or single-stranded. Single-stranded nucleic acid can be the coding strand (sense strand) or the non-coding strand (anti-sense strand).

The invention further provides nucleic acid molecules that encode fragments of the peptides of the present invention as well as nucleic acid molecules that encode obvious variants of the secreted proteins of the present invention that are described above. Such nucleic acid molecules may be naturally occurring, such as allelic variants (same locus), paralogs (different locus), and orthologs (different organism), or may be constructed by recombinant DNA methods or by chemical synthesis. Such non-naturally occurring variants may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells, or organisms. Accordingly, as discussed above, the variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions.

The present invention further provides non-coding fragments of the nucleic acid molecules provided in Figures 1 and 3. Preferred non-coding fragments include, but are not limited to, promoter sequences, enhancer sequences, gene modulating sequences and gene

termination sequences. Such fragments are useful in controlling heterologous gene expression and in developing screens to identify gene-modulating agents. A promoter can readily be identified as being 5' to the ATG start site in the genomic sequence provided in Figure 3.

A fragment comprises a contiguous nucleotide sequence greater than 12 or more nucleotides. Further, a fragment could be at least 30, 40, 50, 100, 250 or 500 nucleotides in length. The length of the fragment will be based on its intended use. For example, the fragment can encode epitope bearing regions of the peptide, or can be useful as DNA probes and primers. Such fragments can be isolated using the known nucleotide sequence to synthesize an oligonucleotide probe. A labeled probe can then be used to screen a cDNA library, genomic DNA library, or mRNA to isolate nucleic acid corresponding to the coding region. Further, primers can be used in PCR reactions to clone specific regions of gene.

A probe/primer typically comprises substantially a purified oligonucleotide or oligonucleotide pair. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 20, 25, 40, 50 or more consecutive nucleotides.

Orthologs, homologs, and allelic variants can be identified using methods well known in the art. As described in the Peptide Section, these variants comprise a nucleotide sequence encoding a peptide that is typically 60-70%, 70-80%, 80-90%, and more typically at least about 90-95% or more homologous to the nucleotide sequence shown in the Figure sheets or a fragment of this sequence. Such nucleic acid molecules can readily be identified as being able to hybridize under moderate to stringent conditions, to the nucleotide sequence shown in the Figure sheets or a fragment of the sequence. Allelic variants can readily be determined by genetic locus of the encoding gene.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences encoding a peptide at least 60-70% homologous to each other typically remain hybridized to each other. The conditions can be such that sequences at least about 60%, at least about 70%, or at least about 80% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found

in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

One example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65C. Examples of moderate to low stringency hybridization conditions are well known in the art.

Nucleic Acid Molecule Uses

The nucleic acid molecules of the present invention are useful for probes, primers, chemical intermediates, and in biological assays. The nucleic acid molecules are useful as a hybridization probe for messenger RNA, transcript/cDNA and genomic DNA to isolate full-length cDNA and genomic clones encoding the peptide described in Figure 2 and to isolate cDNA and genomic clones that correspond to variants (alleles, orthologs, etc.) producing the same or related peptides shown in Figure 2.

The probe can correspond to any sequence along the entire length of the nucleic acid molecules provided in the Figures. Accordingly, it could be derived from 5' noncoding regions, the coding region, and 3' noncoding regions. However, as discussed, fragments are not to be construed as encompassing fragments disclosed prior to the present invention.

The nucleic acid molecules are also useful as primers for PCR to amplify any given region of a nucleic acid molecule and are useful to synthesize antisense molecules of desired length and sequence.

The nucleic acid molecules are also useful for constructing recombinant vectors. Such vectors include expression vectors that express a portion of, or all of, the peptide sequences. Vectors also include insertion vectors, used to integrate into another nucleic acid molecule sequence, such as into the cellular genome, to alter *in situ* expression of a gene and/or gene product. For example, an endogenous coding sequence can be replaced via homologous recombination with all or part of the coding region containing one or more specifically introduced mutations.

The nucleic acid molecules are also useful for expressing antigenic portions of the proteins.

The nucleic acid molecules are also useful as probes for determining the chromosomal positions of the nucleic acid molecules by means of *in situ* hybridization methods.

The nucleic acid molecules are also useful in making vectors containing the gene regulatory regions of the nucleic acid molecules of the present invention.

The nucleic acid molecules are also useful for designing ribozymes corresponding to all, or a part, of the mRNA produced from the nucleic acid molecules described herein.

The nucleic acid molecules are also useful for making vectors that express part, or all, of the peptides.

The nucleic acid molecules are also useful for constructing host cells expressing a part, or all, of the nucleic acid molecules and peptides.

The nucleic acid molecules are also useful for constructing transgenic animals expressing all, or a part, of the nucleic acid molecules and peptides.

The nucleic acid molecules are also useful as hybridization probes for determining the presence, level, form and distribution of nucleic acid expression. Accordingly, the probes can be used to detect the presence of, or to determine levels of, a specific nucleic acid molecule in cells, tissues, and in organisms. The nucleic acid whose level is determined can be DNA or RNA. Accordingly, probes corresponding to the peptides described herein can be used to assess expression and/or gene copy number in a given cell, tissue, or organism. These uses are relevant for diagnosis of disorders involving an increase or decrease in secreted protein expression relative to normal results.

In vitro techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detecting DNA include Southern hybridizations and *in situ* hybridization.

Probes can be used as a part of a diagnostic test kit for identifying cells or tissues that express a secreted protein, such as by measuring a level of a secreted protein-encoding nucleic acid in a sample of cells from a subject e.g., mRNA or genomic DNA, or determining if a secreted protein gene has been mutated.

Nucleic acid expression assays are useful for drug screening to identify compounds that modulate secreted protein nucleic acid expression.

The invention thus provides a method for identifying a compound that can be used to treat a disorder associated with nucleic acid expression of the secreted protein gene, particularly biological and pathological processes that are mediated by the secreted protein in cells and tissues that express it. The method typically includes assaying the ability of the compound to modulate the expression of the secreted protein nucleic acid and thus identifying a compound that can be used to treat a disorder characterized by undesired secreted protein nucleic acid expression. The assays can be performed in cell-based and cell-free systems. Cell-based assays include cells naturally expressing the secreted protein nucleic acid or recombinant cells genetically engineered to express specific nucleic acid sequences.

Thus, modulators of secreted protein gene expression can be identified in a method wherein a cell is contacted with a candidate compound and the expression of mRNA determined. The level of expression of secreted protein mRNA in the presence of the candidate compound is compared to the level of expression of secreted protein mRNA in the absence of the candidate compound. The candidate compound can then be identified as a modulator of nucleic acid expression based on this comparison and be used, for example to treat a disorder characterized by aberrant nucleic acid expression. When expression of mRNA is statistically significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of nucleic acid expression. When nucleic acid expression is statistically significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of nucleic acid expression.

The invention further provides methods of treatment, with the nucleic acid as a target, using a compound identified through drug screening as a gene modulator to modulate secreted protein nucleic acid expression in cells and tissues that express the secreted protein. Modulation includes both up-regulation (i.e. activation or agonization) or down-regulation (suppression or antagonization) or nucleic acid expression.

Alternatively, a modulator for secreted protein nucleic acid expression can be a small molecule or drug identified using the screening assays described herein as long as the drug or small molecule inhibits the secreted protein nucleic acid expression in the cells and tissues that express the protein.

The nucleic acid molecules are also useful for monitoring the effectiveness of modulating compounds on the expression or activity of the secreted protein gene in clinical trials or in a treatment regimen. Thus, the gene expression pattern can serve as a barometer for the continuing effectiveness of treatment with the compound, particularly with compounds to which a patient can develop resistance. The gene expression pattern can also serve as a marker indicative of a physiological response of the affected cells to the compound. Accordingly, such monitoring would allow either increased administration of the compound or the administration of alternative compounds to which the patient has not become resistant. Similarly, if the level of nucleic acid expression falls below a desirable level, administration of the compound could be commensurately decreased.

The nucleic acid molecules are also useful in diagnostic assays for qualitative changes in secreted protein nucleic acid expression, and particularly in qualitative changes that lead to pathology. The nucleic acid molecules can be used to detect mutations in secreted protein genes and gene expression products such as mRNA. The nucleic acid molecules can be used as hybridization probes to detect naturally occurring genetic mutations in the secreted protein gene and thereby to determine whether a subject with the mutation is at risk for a disorder caused by the mutation. Mutations include deletion, addition, or substitution of one or more nucleotides in the gene, chromosomal rearrangement, such as inversion or transposition, modification of genomic DNA, such as aberrant methylation patterns or changes in gene copy number, such as amplification. Detection of a mutated form of the secreted protein gene associated with a dysfunction provides a diagnostic tool for an active disease or susceptibility to disease when the disease results from overexpression, underexpression, or altered expression of a secreted protein.

Individuals carrying mutations in the secreted protein gene can be detected at the nucleic acid level by a variety of techniques. Genomic DNA can be analyzed directly or can be amplified by using PCR prior to analysis. RNA or cDNA can be used in the same way. In some uses, detection of the mutation involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.*, *Science* 241:1077-1080 (1988); and Nakazawa *et al.*, *PNAS* 91:360-364 (1994)), the latter of which can be particularly useful for detecting point mutations in the

gene (see Abravaya *et al.*, *Nucleic Acids Res.* 23:675-682 (1995)). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a gene under conditions such that hybridization and amplification of the gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. Deletions and insertions can be detected by a change in size of the amplified product compared to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to normal RNA or antisense DNA sequences.

Alternatively, mutations in a secreted protein gene can be directly identified, for example, by alterations in restriction enzyme digestion patterns determined by gel electrophoresis.

Further, sequence-specific ribozymes (U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site. Perfectly matched sequences can be distinguished from mismatched sequences by nuclease cleavage digestion assays or by differences in melting temperature.

Sequence changes at specific locations can also be assessed by nuclease protection assays such as RNase and S1 protection or the chemical cleavage method. Furthermore, sequence differences between a mutant secreted protein gene and a wild-type gene can be determined by direct DNA sequencing. A variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve, C.W., (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO 94/16101; Cohen *et al.*, *Adv. Chromatogr.* 36:127-162 (1996); and Griffin *et al.*, *Appl. Biochem. Biotechnol.* 38:147-159 (1993)).

Other methods for detecting mutations in the gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA duplexes (Myers *et al.*, *Science* 230:1242 (1985)); Cotton *et al.*, *PNAS* 85:4397 (1988); Saleeba *et al.*, *Meth. Enzymol.* 217:286-295 (1992)), electrophoretic mobility of mutant and wild type nucleic acid is compared (Orita *et al.*, *PNAS* 86:2766 (1989); Cotton *et al.*, *Mutat. Res.* 285:125-144 (1993); and Hayashi *et al.*, *Genet. Anal. Tech. Appl.* 9:73-79

(1992)), and movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (Myers *et al.*, *Nature* 313:495 (1985)). Examples of other techniques for detecting point mutations include selective oligonucleotide hybridization, selective amplification, and selective primer extension.

The nucleic acid molecules are also useful for testing an individual for a genotype that while not necessarily causing the disease, nevertheless affects the treatment modality. Thus, the nucleic acid molecules can be used to study the relationship between an individual's genotype and the individual's response to a compound used for treatment (pharmacogenomic relationship). Accordingly, the nucleic acid molecules described herein can be used to assess the mutation content of the secreted protein gene in an individual in order to select an appropriate compound or dosage regimen for treatment.

Thus nucleic acid molecules displaying genetic variations that affect treatment provide a diagnostic target that can be used to tailor treatment in an individual. Accordingly, the production of recombinant cells and animals containing these polymorphisms allow effective clinical design of treatment compounds and dosage regimens.

The nucleic acid molecules are thus useful as antisense constructs to control secreted protein gene expression in cells, tissues, and organisms. A DNA antisense nucleic acid molecule is designed to be complementary to a region of the gene involved in transcription, preventing transcription and hence production of secreted protein. An antisense RNA or DNA nucleic acid molecule would hybridize to the mRNA and thus block translation of mRNA into secreted protein.

Alternatively, a class of antisense molecules can be used to inactivate mRNA in order to decrease expression of secreted protein nucleic acid. Accordingly, these molecules can treat a disorder characterized by abnormal or undesired secreted protein nucleic acid expression. This technique involves cleavage by means of ribozymes containing nucleotide sequences complementary to one or more regions in the mRNA that attenuate the ability of the mRNA to be translated. Possible regions include coding regions and particularly coding regions corresponding to the catalytic and other functional activities of the secreted protein, such as substrate binding.

The nucleic acid molecules also provide vectors for gene therapy in patients containing cells that are aberrant in secreted protein gene expression. Thus, recombinant cells, which include the patient's cells that have been engineered *ex vivo* and returned to the patient, are introduced into an individual where the cells produce the desired secreted protein to treat the individual.

The invention also encompasses kits for detecting the presence of a secreted protein nucleic acid in a biological sample. For example, the kit can comprise reagents such as a labeled or labelable nucleic acid or agent capable of detecting secreted protein nucleic acid in a biological sample; means for determining the amount of secreted protein nucleic acid in the sample; and means for comparing the amount of secreted protein nucleic acid in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect secreted protein mRNA or DNA.

Nucleic Acid Arrays

The present invention further provides nucleic acid detection kits, such as arrays or microarrays of nucleic acid molecules that are based on the sequence information provided in Figures 1 and 3 (SEQ ID NOS:1 and 3).

As used herein "Arrays" or "Microarrays" refers to an array of distinct polynucleotides or oligonucleotides synthesized on a substrate, such as paper, nylon or other type of membrane, filter, chip, glass slide, or any other suitable solid support. In one embodiment, the microarray is prepared and used according to the methods described in US Patent 5,837,832, Chee *et al.*, PCT application W095/11995 (Chee *et al.*), Lockhart, D. J. *et al.* (1996; Nat. Biotech. 14: 1675-1680) and Schena, M. *et al.* (1996; Proc. Natl. Acad. Sci. 93: 10614-10619), all of which are incorporated herein in their entirety by reference. In other embodiments, such arrays are produced by the methods described by Brown *et al.*, US Patent No. 5,807,522.

The microarray or detection kit is preferably composed of a large number of unique, single-stranded nucleic acid sequences, usually either synthetic antisense oligonucleotides or fragments of cDNAs, fixed to a solid support. The oligonucleotides are preferably about 6-60 nucleotides in length, more preferably 15-30 nucleotides in

length, and most preferably about 20-25 nucleotides in length. For a certain type of microarray or detection kit, it may be preferable to use oligonucleotides that are only 7-20 nucleotides in length. The microarray or detection kit may contain oligonucleotides that cover the known 5', or 3', sequence, sequential oligonucleotides which cover the full length sequence; or unique oligonucleotides selected from particular areas along the length of the sequence. Polynucleotides used in the microarray or detection kit may be oligonucleotides that are specific to a gene or genes of interest.

In order to produce oligonucleotides to a known sequence for a microarray or detection kit, the gene(s) of interest (or an ORF identified from the contigs of the present invention) is typically examined using a computer algorithm which starts at the 5' or at the 3' end of the nucleotide sequence. Typical algorithms will then identify oligomers of defined length that are unique to the gene, have a GC content within a range suitable for hybridization, and lack predicted secondary structure that may interfere with hybridization. In certain situations it may be appropriate to use pairs of oligonucleotides on a microarray or detection kit. The "pairs" will be identical, except for one nucleotide that preferably is located in the center of the sequence. The second oligonucleotide in the pair (mismatched by one) serves as a control. The number of oligonucleotide pairs may range from two to one million. The oligomers are synthesized at designated areas on a substrate using a light-directed chemical process. The substrate may be paper, nylon or other type of membrane, filter, chip, glass slide or any other suitable solid support.

In another aspect, an oligonucleotide may be synthesized on the surface of the substrate by using a chemical coupling procedure and an ink jet application apparatus, as described in PCT application W095/251116 (Baldeschweiler *et al.*) which is incorporated herein in its entirety by reference. In another aspect, a "gridded" array analogous to a dot (or slot) blot may be used to arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a vacuum system, thermal, UV, mechanical or chemical bonding procedures. An array, such as those described above, may be produced by hand or by using available devices (slot blot or dot blot apparatus), materials (any suitable solid support), and machines (including robotic instruments), and may contain 8, 24, 96, 384, 1536, 6144 or more oligonucleotides, or any other number between two and one million which lends itself to the efficient use of commercially available instrumentation.

In order to conduct sample analysis using a microarray or detection kit, the RNA or DNA from a biological sample is made into hybridization probes. The mRNA is isolated, and cDNA is produced and used as a template to make antisense RNA (aRNA). The aRNA is amplified in the presence of fluorescent nucleotides, and labeled probes are incubated with the microarray or detection kit so that the probe sequences hybridize to complementary oligonucleotides of the microarray or detection kit. Incubation conditions are adjusted so that hybridization occurs with precise complementary matches or with various degrees of less complementarity. After removal of nonhybridized probes, a scanner is used to determine the levels and patterns of fluorescence. The scanned images are examined to determine degree of complementarity and the relative abundance of each oligonucleotide sequence on the microarray or detection kit. The biological samples may be obtained from any bodily fluids (such as blood, urine, saliva, phlegm, gastric juices, etc.), cultured cells, biopsies, or other tissue preparations. A detection system may be used to measure the absence, presence, and amount of hybridization for all of the distinct sequences simultaneously. This data may be used for large-scale correlation studies on the sequences, expression patterns, mutations, variants, or polymorphisms among samples.

Using such arrays, the present invention provides methods to identify the expression of the secreted proteins/peptides of the present invention. In detail, such methods comprise incubating a test sample with one or more nucleic acid molecules and assaying for binding of the nucleic acid molecule with components within the test sample. Such assays will typically involve arrays comprising many genes, at least one of which is a gene of the present invention and or alleles of the secreted protein gene of the present invention.

Conditions for incubating a nucleic acid molecule with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid molecule used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or array assay formats can readily be adapted to employ the novel fragments of the Human genome disclosed herein. Examples of such assays can be found in Chard, T, *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier

Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The test samples of the present invention include cells, protein or membrane extracts of cells. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing nucleic acid extracts or of cells are well known in the art and can be readily be adapted in order to obtain a sample that is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the nucleic acid molecules that can bind to a fragment of the Human genome disclosed herein; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound nucleic acid.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers, strips of plastic, glass or paper, or arraying material such as silica. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the nucleic acid probe, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound probe. One skilled in the art will readily recognize that the previously unidentified secreted protein gene of the present invention can be routinely identified using the sequence information disclosed herein can be readily incorporated

into one of the established kit formats which are well known in the art, particularly expression arrays.

Vectors/host cells

The invention also provides vectors containing the nucleic acid molecules described herein. The term "vector" refers to a vehicle, preferably a nucleic acid molecule, which can transport the nucleic acid molecules. When the vector is a nucleic acid molecule, the nucleic acid molecules are covalently linked to the vector nucleic acid. With this aspect of the invention, the vector includes a plasmid, single or double stranded phage, a single or double stranded RNA or DNA viral vector, or artificial chromosome, such as a BAC, PAC, YAC, or MAC.

A vector can be maintained in the host cell as an extrachromosomal element where it replicates and produces additional copies of the nucleic acid molecules. Alternatively, the vector may integrate into the host cell genome and produce additional copies of the nucleic acid molecules when the host cell replicates.

The invention provides vectors for the maintenance (cloning vectors) or vectors for expression (expression vectors) of the nucleic acid molecules. The vectors can function in prokaryotic or eukaryotic cells or in both (shuttle vectors).

Expression vectors contain cis-acting regulatory regions that are operably linked in the vector to the nucleic acid molecules such that transcription of the nucleic acid molecules is allowed in a host cell. The nucleic acid molecules can be introduced into the host cell with a separate nucleic acid molecule capable of affecting transcription. Thus, the second nucleic acid molecule may provide a trans-acting factor interacting with the cis-regulatory control region to allow transcription of the nucleic acid molecules from the vector. Alternatively, a trans-acting factor may be supplied by the host cell. Finally, a trans-acting factor can be produced from the vector itself. It is understood, however, that in some embodiments, transcription and/or translation of the nucleic acid molecules can occur in a cell-free system.

The regulatory sequence to which the nucleic acid molecules described herein can be operably linked include promoters for directing mRNA transcription. These include, but are not limited to, the left promoter from bacteriophage λ , the lac, TRP, and TAC promoters

from *E. coli*, the early and late promoters from SV40, the CMV immediate early promoter, the adenovirus early and late promoters, and retrovirus long-terminal repeats.

In addition to control regions that promote transcription, expression vectors may also include regions that modulate transcription, such as repressor binding sites and enhancers. Examples include the SV40 enhancer, the cytomegalovirus immediate early enhancer, polyoma enhancer, adenovirus enhancers, and retrovirus LTR enhancers.

In addition to containing sites for transcription initiation and control, expression vectors can also contain sequences necessary for transcription termination and, in the transcribed region a ribosome binding site for translation. Other regulatory control elements for expression include initiation and termination codons as well as polyadenylation signals. The person of ordinary skill in the art would be aware of the numerous regulatory sequences that are useful in expression vectors. Such regulatory sequences are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*. 2nd. ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (1989).

A variety of expression vectors can be used to express a nucleic acid molecule. Such vectors include chromosomal, episomal, and virus-derived vectors, for example vectors derived from bacterial plasmids, from bacteriophage, from yeast episomes, from yeast chromosomal elements, including yeast artificial chromosomes, from viruses such as baculoviruses, papovaviruses such as SV40, Vaccinia viruses, adenoviruses, poxviruses, pseudorabies viruses, and retroviruses. Vectors may also be derived from combinations of these sources such as those derived from plasmid and bacteriophage genetic elements, e.g. cosmids and phagemids. Appropriate cloning and expression vectors for prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*. 2nd. ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (1989).

The regulatory sequence may provide constitutive expression in one or more host cells (i.e. tissue specific) or may provide for inducible expression in one or more cell types such as by temperature, nutrient additive, or exogenous factor such as a hormone or other ligand. A variety of vectors providing for constitutive and inducible expression in prokaryotic and eukaryotic hosts are well known to those of ordinary skill in the art.

The nucleic acid molecules can be inserted into the vector nucleic acid by well-known methodology. Generally, the DNA sequence that will ultimately be expressed is

joined to an expression vector by cleaving the DNA sequence and the expression vector with one or more restriction enzymes and then ligating the fragments together. Procedures for restriction enzyme digestion and ligation are well known to those of ordinary skill in the art.

The vector containing the appropriate nucleic acid molecule can be introduced into an appropriate host cell for propagation or expression using well-known techniques. Bacterial cells include, but are not limited to, *E. coli*, *Streptomyces*, and *Salmonella typhimurium*. Eukaryotic cells include, but are not limited to, yeast, insect cells such as *Drosophila*, animal cells such as COS and CHO cells, and plant cells.

As described herein, it may be desirable to express the peptide as a fusion protein. Accordingly, the invention provides fusion vectors that allow for the production of the peptides. Fusion vectors can increase the expression of a recombinant protein, increase the solubility of the recombinant protein, and aid in the purification of the protein by acting for example as a ligand for affinity purification. A proteolytic cleavage site may be introduced at the junction of the fusion moiety so that the desired peptide can ultimately be separated from the fusion moiety. Proteolytic enzymes include, but are not limited to, factor Xa, thrombin, and enterokinase. Typical fusion expression vectors include pGEX (Smith *et al.*, *Gene* 67:31-40 (1988)), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, *Gene* 69:301-315 (1988)) and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185:60-89 (1990)).

Recombinant protein expression can be maximized in host bacteria by providing a genetic background wherein the host cell has an impaired capacity to proteolytically cleave the recombinant protein. (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Alternatively, the sequence of the nucleic acid molecule of interest can be altered to provide preferential codon usage for a specific host cell, for example *E. coli*. (Wada *et al.*, *Nucleic Acids Res.* 20:2111-2118 (1992)).

The nucleic acid molecules can also be expressed by expression vectors that are operative in yeast. Examples of vectors for expression in yeast e.g., *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, *EMBO J.* 6:229-234 (1987)), pMFa (Kurjan *et al.*, *Cell* 30:933-943(1982)), pJRY88 (Schultz *et al.*, *Gene* 54:113-123 (1987)), and pYES2 (Invitrogen Corporation, San Diego, CA).

The nucleic acid molecules can also be expressed in insect cells using, for example, baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.*, *Mol. Cell Biol.* 3:2156-2165 (1983)) and the pVL series (Lucklow *et al.*, *Virology* 170:31-39 (1989)).

In certain embodiments of the invention, the nucleic acid molecules described herein are expressed in mammalian cells using mammalian expression vectors. Examples of mammalian expression vectors include pCDM8 (Seed, B. *Nature* 329:840(1987)) and pMT2PC (Kaufman *et al.*, *EMBO J.* 6:187-195 (1987)).

The expression vectors listed herein are provided by way of example only of the well-known vectors available to those of ordinary skill in the art that would be useful to express the nucleic acid molecules. The person of ordinary skill in the art would be aware of other vectors suitable for maintenance propagation or expression of the nucleic acid molecules described herein. These are found for example in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

The invention also encompasses vectors in which the nucleic acid sequences described herein are cloned into the vector in reverse orientation, but operably linked to a regulatory sequence that permits transcription of antisense RNA. Thus, an antisense transcript can be produced to all, or to a portion, of the nucleic acid molecule sequences described herein, including both coding and non-coding regions. Expression of this antisense RNA is subject to each of the parameters described above in relation to expression of the sense RNA (regulatory sequences, constitutive or inducible expression, tissue-specific expression).

The invention also relates to recombinant host cells containing the vectors described herein. Host cells therefore include prokaryotic cells, lower eukaryotic cells such as yeast,

other eukaryotic cells such as insect cells, and higher eukaryotic cells such as mammalian cells.

The recombinant host cells are prepared by introducing the vector constructs described herein into the cells by techniques readily available to the person of ordinary skill in the art. These include, but are not limited to, calcium phosphate transfection, DEAE-dextran-mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, lipofection, and other techniques such as those found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Host cells can contain more than one vector. Thus, different nucleotide sequences can be introduced on different vectors of the same cell. Similarly, the nucleic acid molecules can be introduced either alone or with other nucleic acid molecules that are not related to the nucleic acid molecules such as those providing trans-acting factors for expression vectors. When more than one vector is introduced into a cell, the vectors can be introduced independently, co-introduced or joined to the nucleic acid molecule vector.

In the case of bacteriophage and viral vectors, these can be introduced into cells as packaged or encapsulated virus by standard procedures for infection and transduction. Viral vectors can be replication-competent or replication-defective. In the case in which viral replication is defective, replication will occur in host cells providing functions that complement the defects.

Vectors generally include selectable markers that enable the selection of the subpopulation of cells that contain the recombinant vector constructs. The marker can be contained in the same vector that contains the nucleic acid molecules described herein or may be on a separate vector. Markers include tetracycline or ampicillin-resistance genes for prokaryotic host cells and dihydrofolate reductase or neomycin resistance for eukaryotic host cells. However, any marker that provides selection for a phenotypic trait will be effective.

While the mature proteins can be produced in bacteria, yeast, mammalian cells, and other cells under the control of the appropriate regulatory sequences, cell- free transcription and translation systems can also be used to produce these proteins using RNA derived from the DNA constructs described herein.

Where secretion of the peptide is desired, which is difficult to achieve with multi-transmembrane domain containing proteins such as kinases, appropriate secretion signals are incorporated into the vector. The signal sequence can be endogenous to the peptides or heterologous to these peptides.

Where the peptide is not secreted into the medium, which is typically the case with kinases, the protein can be isolated from the host cell by standard disruption procedures, including freeze thaw, sonication, mechanical disruption, use of lysing agents and the like. The peptide can then be recovered and purified by well-known purification methods including ammonium sulfate precipitation, acid extraction, anion or cationic exchange chromatography, phosphocellulose chromatography, hydrophobic-interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, or high performance liquid chromatography.

It is also understood that depending upon the host cell in recombinant production of the peptides described herein, the peptides can have various glycosylation patterns, depending upon the cell, or maybe non-glycosylated as when produced in bacteria. In addition, the peptides may include an initial modified methionine in some cases as a result of a host-mediated process.

Uses of vectors and host cells

The recombinant host cells expressing the peptides described herein have a variety of uses. First, the cells are useful for producing a secreted protein or peptide that can be further purified to produce desired amounts of secreted protein or fragments. Thus, host cells containing expression vectors are useful for peptide production.

Host cells are also useful for conducting cell-based assays involving the secreted protein or secreted protein fragments, such as those described above as well as other formats known in the art. Thus, a recombinant host cell expressing a native secreted protein is useful for assaying compounds that stimulate or inhibit secreted protein function.

Host cells are also useful for identifying secreted protein mutants in which these functions are affected. If the mutants naturally occur and give rise to a pathology, host cells containing the mutations are useful to assay compounds that have a desired effect on the

mutant secreted protein (for example, stimulating or inhibiting function) which may not be indicated by their effect on the native secreted protein.

Genetically engineered host cells can be further used to produce non-human transgenic animals. A transgenic animal is preferably a mammal, for example a rodent, such as a rat or mouse, in which one or more of the cells of the animal include a transgene. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal in one or more cell types or tissues of the transgenic animal. These animals are useful for studying the function of a secreted protein and identifying and evaluating modulators of secreted protein activity. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, and amphibians.

A transgenic animal can be produced by introducing nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Any of the secreted protein nucleotide sequences can be introduced as a transgene into the genome of a non-human animal, such as a mouse.

Any of the regulatory or other sequences useful in expression vectors can form part of the transgenic sequence. This includes intronic sequences and polyadenylation signals, if not already included. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the secreted protein to particular cells.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, both by Leder *et al.*, U.S. Patent No. 4,873,191 by Wagner *et al.* and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of transgenic mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene can further be bred to other transgenic animals carrying other transgenes. A transgenic animal also includes animals in which the entire animal or tissues

in the animal have been produced using the homologously recombinant host cells described herein.

In another embodiment, transgenic non-human animals can be produced which contain selected systems that allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso *et al. PNAS* 89:6232-6236 (1992). Another example of a recombinase system is the FLP recombinase system of *S. cerevisiae* (O'Gorman *et al. Science* 251:1351-1355 (1991)). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein is required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, I. *et al. Nature* 385:810-813 (1997) and PCT International Publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyst and then transferred to pseudopregnant female foster animal. The offspring born of this female foster animal will be a clone of the animal from which the cell, e.g., the somatic cell, is isolated.

Transgenic animals containing recombinant cells that express the peptides described herein are useful to conduct the assays described herein in an *in vivo* context. Accordingly, the various physiological factors that are present *in vivo* and that could effect substrate binding, secreted protein activation, and signal transduction, may not be evident from *in vitro* cell-free or cell-based assays. Accordingly, it is useful to provide non-human transgenic animals to assay *in vivo* secreted protein function, including substrate interaction, the effect of specific mutant secreted proteins on secreted protein function and substrate interaction, and the effect of chimeric secreted proteins. It is also possible to assess the

effect of null mutations, that is, mutations that substantially or completely eliminate one or more secreted protein functions.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

Claims

That which is claimed is:

1. An isolated peptide consisting of an amino acid sequence selected from the group consisting of:

- (a) an amino acid sequence shown in SEQ ID NO:2;
- (b) an amino acid sequence of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;
- (c) an amino acid sequence of an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3; and
- (d) a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids.

2. An isolated peptide comprising an amino acid sequence selected from the group consisting of:

- (a) an amino acid sequence shown in SEQ ID NO:2;
- (b) an amino acid sequence of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;
- (c) an amino acid sequence of an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3; and
- (d) a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids.

3. An isolated antibody that selectively binds to a peptide of claim 2.

4. An isolated nucleic acid molecule consisting of a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence that encodes an amino acid sequence shown in SEQ ID NO:2;

(b) a nucleotide sequence that encodes of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said nucleotide sequence hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(c) a nucleotide sequence that encodes an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said nucleotide sequence hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(d) a nucleotide sequence that encodes a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids; and

(e) a nucleotide sequence that is the complement of a nucleotide sequence of (a)-(d).

5. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence that encodes an amino acid sequence shown in SEQ ID NO:2;

(b) a nucleotide sequence that encodes of an allelic variant of an amino acid sequence shown in SEQ ID NO:2, wherein said nucleotide sequence hybridizes under stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(c) a nucleotide sequence that encodes an ortholog of an amino acid sequence shown in SEQ ID NO:2, wherein said nucleotide sequence hybridizes under

stringent conditions to the opposite strand of a nucleic acid molecule shown in SEQ ID NOS:1 or 3;

(d) a nucleotide sequence that encodes a fragment of an amino acid sequence shown in SEQ ID NO:2, wherein said fragment comprises at least 10 contiguous amino acids; and

(e) a nucleotide sequence that is the complement of a nucleotide sequence of (a)-(d).

6. A gene chip comprising a nucleic acid molecule of claim 5.

7. A transgenic non-human animal comprising a nucleic acid molecule of claim 5.

8. A nucleic acid vector comprising a nucleic acid molecule of claim 5.

9. A host cell containing the vector of claim 8.

10. A method for producing any of the peptides of claim 1 comprising introducing a nucleotide sequence encoding any of the amino acid sequences in (a)-(d) into a host cell, and culturing the host cell under conditions in which the peptides are expressed from the nucleotide sequence.

11. A method for producing any of the peptides of claim 2 comprising introducing a nucleotide sequence encoding any of the amino acid sequences in (a)-(d) into a host cell, and culturing the host cell under conditions in which the peptides are expressed from the nucleotide sequence.

12. A method for detecting the presence of any of the peptides of claim 2 in a sample, said method comprising contacting said sample with a detection agent that specifically allows detection of the presence of the peptide in the sample and then detecting the presence of the peptide.

13. A method for detecting the presence of a nucleic acid molecule of claim 5 in a sample, said method comprising contacting the sample with an oligonucleotide that hybridizes to said nucleic acid molecule under stringent conditions and determining whether the oligonucleotide binds to said nucleic acid molecule in the sample.

14. A method for identifying a modulator of a peptide of claim 2, said method comprising contacting said peptide with an agent and determining if said agent has modulated the function or activity of said peptide.

15. The method of claim 14, wherein said agent is administered to a host cell comprising an expression vector that expresses said peptide.

16. A method for identifying an agent that binds to any of the peptides of claim 2, said method comprising contacting the peptide with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the peptide.

17. A pharmaceutical composition comprising an agent identified by the method of claim 16 and a pharmaceutically acceptable carrier therefor.

18. A method for treating a disease or condition mediated by a human secreted protein, said method comprising administering to a patient a pharmaceutically effective amount of an agent identified by the method of claim 16.

19. A method for identifying a modulator of the expression of a peptide of claim 2, said method comprising contacting a cell expressing said peptide with an agent, and determining if said agent has modulated the expression of said peptide.

20. An isolated human secreted peptide having an amino acid sequence that shares at least 70% homology with an amino acid sequence shown in SEQ ID NO:2.

21. A peptide according to claim 20 that shares at least 90 percent homology with an amino acid sequence shown in SEQ ID NO:2.

22. An isolated nucleic acid molecule encoding a human secreted peptide, said nucleic acid molecule sharing at least 80 percent homology with a nucleic acid molecule shown in SEQ ID NOS:1 or 3.

23. A nucleic acid molecule according to claim 22 that shares at least 90 percent homology with a nucleic acid molecule shown in SEQ ID NOS:1 or 3.

ABSTRACT

The present invention provides amino acid sequences of peptides that are encoded by genes within the human genome, the secreted peptides of the present invention. The present invention specifically provides isolated peptide and nucleic acid molecules, methods of identifying orthologs and paralogs of the secreted peptides, and methods of identifying modulators of the secreted peptides.

```

1   ATGGGACCCT GGTCA GTGGT GGTGCTGGT TGC GG CATGA AGCAGCTGGG
51  GCAGGCCCTC CAGGCCTCAG TTTCCCTGTC TATCATCACA GAGAATCAGG
101 GCAAAAGGTG TCCCTTCTGT GGAGCCCAGA ACCTGATGAC CTGTCAGAAAT
151 CCCACCCTTC CTTCTGTCTC CCATCGAAGT CCTCCAGGAA ATGCAGCTGT
201 TTCAGTGACA GGGGGTGATT GCCATCTTCC AACTGAGGAG GAATTTGGGG
251 TTTTGGTCCA GTCCATGAAG TGTGACACAG TCAGAATAAA AGGCGTCCTT
301 CAAGGCCCTA CCACAGCCCC TCCTCTCATG ACCAGTGAAG GCAATGTAAC
351 TGCAGAAGAC ACTGAGGAGG CAATTCGGGC TTTTGTGTAC GCTGTGGCTG
401 CTGCTTCTGC TGCCGAAGCT TGGCATTGGA GACACCTCGT CCTCCTCTCA
451 GGACAGATCC ATGAACCCAT CGGCAGCGGC GGAATATAA TCAACACTAA
501 TAAAGGAGGA AGGAGCTGTC AGAATCCTGC CCTTCCGTCT CCAGATCAAA
551 GTCCTTCAGG AAATGCAACT ACTTCAGTGA CAAGAGATAA TTATCATCTT
601 CTGACAGAGG AGGAATTTGG GGTTTGGTCC CAGTCCATGA AGTGGCACAG
651 TCAGAATAAA AGTGGCGGGA GCGTCCCGT GAGAGGCCCG ACCCAGGAGC
701 CATGTTCTGA ATCTCAAATT TTGAAAGAAT CTTTGTGTCCC ACCCACAACA
751 CCCAAAGAAA ATAATAAACA GGAGAGGGAG GATGAAAATT GGCGTCTACC
801 ACCCCCTCCA GTAGCAGAAA CACCTGTACC ATCTCCTTCA GTAACAGAAA
851 TAGAGACCCC ACTGCAAAGA ATTCCGCGGA CTGCTACCAT AGCTGGAGAG
901 CCCTTAGGAC ATTGCACTTT CACTATTTCT CCGGCATTTCG TACATTCTGT
951 GCTCAACAAA CGGAAGCGGC AGCTGGAGCT GCTGCTCCGG GAGGTGGAGT
1001 GGCCTGGCAG AGGGCACATG GCTGCCACCT GCTGCAAGCT CCAGGTAGAA
1051 GGGCAGGACA GAACCATGAG CCTAGCGGCA GCGCCGGTTC GCGAAGCTCC
1101 CCCTCCGCCA ACGGGCGCCT CCTCAGAGCC GTCCGTGCCC GCCCTGCCGG
1151 GAGCTGACCC GCAGCGCAGT GCAGAGTTGC TCCTGTTGGC GGTGACCAGG
1201 GAGGGACTGG AGCGCGGAT CATCTCCAGG AAGCGGGCTG AGTAG

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FEATURES:

Start codon: 1
Stop codon: 1243

Homologous proteins:

EST:

Blast hits:

	Score	E
CRA 3000001473333 /altid=gi 1186824 /dataset=dbest /taxon=9606 ...	159	2e-36

FIGURE 1

```

1  MGPWSVVVLV CGMKQLGQAL QASVLSIIT ENQGKRCPCF GAQNLMTCQN
51 PTLPSVSHRS PPGNAAVSVT GGDCHLPTEE EFGVLVQSMK CDTVRIKGV
101 QGPTTAPPLM TSEGNVTAED TEEAIRAFVY AVAAASAAEA WHWRHLVLLS
151 GQIHEPIGSG GNIINTNKGK RSCQNPALPS PDQSPSGNAT TSVTRDNYHL
201 LTEEEFGVWS QSMKWHSONK SGGSPVVRGP TQEPCESESI LKESFVPPTT
251 PKENNKQERE DENWRLPPPP VAETPVPSPS VTEIETPLQR IPRTATIAGE
301 PLGHCTFTIS PAFVHSVNLK RKRQLELLLR EVEWPGRGHM AATCCKLQVE
351 GQDRTMSLAA APVREAPPPP TGASSEPSVP ALPGADPQRS AELLLLAVTR
401 EGLERRIISR KRAE

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FEATURES:

Functional domains and key regions:

BLAST Alignment to Top Hit:

Hmmer results:

Model	Description	Score	E-value	N
PF00947	Picornavirus core protein 2A	4.3	5.6	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00947	1/1	197	205 ..	1	9 [.	4.3	5.6

FIGURE 2

1	AGCCAGACTA	GGAGTGAGCC	AGAAGAGGGG	AAGGATGGTG	GAGGCACAGG
51	CTGCACTCTA	CTGGTGCCCC	AGACCCAGAC	TGCATGCCCA	GGCTGCAGTC
101	CAAAGGATAC	TCGGTGCGGG	TCCCTGTCCC	CCATAGCATC	TTAGATCAGC
151	TGCTGAGGCT	GGAGCTTCTT	CCATTCCTTG	AGCATCAGGG	GTGTGTATCA
201	TTTCCAAGGG	TTTTTCAGACA	ATCCCTGGTG	ACCCCTGGCA	GGGGCGGGTT
251	ATCATGGCGA	TCGGTCCATG	GCCTTGCCCTC	CAAGCAGCAC	CCAGCAATCC
301	CCATGCCAC	CAATGCACTA	AATGTTTGTG	GTGGGCCTCT	TTCTGGAAGC
351	TCACCTTCTC	CTCCTGTTTG	CCCTCCATCT	TCCCCAAACC	AGTACTTCTG
401	GCCATCCTCC	TTGTCACCAC	AATGGGAAAA	CTGGGTCCTG	GAGACTCAGA
451	AACCACTGTG	CAGGCCTCGA	GTCTTCCCCT	GTCCTGGCTA	ACAGGGCATG
501	GAATCAGAGA	GAAAAGTCAT	CTTCCACCTC	CTGAAGGCTG	CCAGCGTCAG
551	GGCTTGGCAC	ACTGAGGCTG	ACAGGGGCCT	TCTGAAGGCC	AGAGGAGATG
601	GCCCCGGACA	TAAGGCTGAA	GCAACCTGTC	TGAGCCAAAG	ATCTGTTTGT
651	GTCTCCTGA	ATCTTAGTGG	CCTTCTAAAG	GCGGGTGTGA	TCAGCCATGG
701	GTCATCAGAGA	CAGTGGAGTC	CAGTAGCTGC	TAGGTGGGAC	ACGGGCACAA
751	TTTCACTTGC	AGACCAGCTG	CACGGAGTGG	ATAAAGAGAG	AGTTCTGTGT
801	GGGAATCTCC	TTTGGTGGAT	CATCAGGGAG	GTGAAGTCTT	TGTCATAGCC
851	TCATATCCAG	CTTGTGTGAT	ACCAATTCCA	GTGAAGCTGG	AACAAGCTGG
901	CACTGCTCAA	ACAGGCCCTAC	CAAGACATCA	TGTTTTTTTT	TTTTTTTTTCC
951	ACCAAACCTG	GACCTGAATG	GGGATGTGGA	CACACATAGA	GTCCAGAGGA
1001	TGGGACCCCTG	GTCAGTGGTG	GTGCTGGTGT	GCGGCATGAA	GCAGCTGGGG
1051	CAGGCCCTCC	AGGTGGGAGG	AGGAGCCAGC	CTCTCCTGTG	GGGTCTGGG
1101	CAAGTCATTT	CCCTCCTTGA	CGCTCTGTTT	CCTCATCTGG	AAAATCCAGG
1151	AAGCCTGTTG	TGCAGTCTC	AGAGGGTCAT	GATAAGGTGC	AAAGGAGGAA
1201	GAAATTTTGA	GAGTTCTTGT	GCCTTCCTCT	TCCTGAGAGG	GATGATGGTG
1251	AGAACAGTGT	GGATAACCAC	ATGCAACTGA	GTCCCCAAAA	GGCCCTGTGA
1301	GGAAGGTGTT	GTTCCTCATGA	TGCTTCCCAG	ATGAGGAAAC	AGTCTCAGGG
1351	AGGCCTGGCT	GCATGCCCAA	GGGTACACA	CACACTGAAT	GTTGGAGCTG
1401	GGAGTAAATC	TAGAGTCAGG	GCTCACTGGA	GGTGGTGGGA	GCATTGCACC
1451	AGCTGCCTCA	TGCAGTTATC	CAAGATCTGA	GGTCAGGGGT	CTGGGGTATA
1501	ACTCGGTGAG	AGAACCACAG	TCTCACTGAC	CCTGTTTCTG	ACTCTGCTAG
1551	GTAGGGAAC	TTTTAGAGTC	CAGATGCTGC	TGTTGCTGCT	CCAGGGAGTT
1601	AAGGACAGGG	CTTTCCCTC	CCAGCTGGAG	TTCTCCACAT	CAAGAGACCA
1651	GAGTGTCTTC	CTCCTCTAGC	CCTGCCCTCC	TGTGGCCACA	GTACTTGGAA
1701	TGCCTTCATT	AACGTGACCA	GAGAAAGAGA	CTTAGAGAGC	TGAGTTCACA
1751	GTGGATTGGG	AAAAGAGTGA	GGCTGGGGAC	AACCTGACTT	TGTGACTTAT
1801	TAAAATCCTA	CCTTAGAGTT	AACTAGAAAG	AGCTTGGTGT	CTTTGGAGGC
1851	CAGCTGTGGA	AAGAGGAGGT	AAAGATGTCT	TGTAAGGAGG	CTGAGGGTCC
1901	TTGGCTGCTC	CAAGTGGGAG	ACTTGGGTAG	GGGCGTCAAG	GAGACATGGG
1951	TTGGTGAGAG	TTCAAAGGAC	AGGCCTTATG	CAGGAAGCTG	AGAATTGTGT
2001	CTCATCACTG	CTACCACCTT	GGAGGAACAG	GGAGCTGTAC	CCTCTCTCGG
2051	CACACTTCTC	ACTGACCTGA	TGATGCTGGA	CATTGCCATA	GAGGATTATA
2101	ATGATGTGTG	TGACACTGGG	GCAGGCAGGC	AGTTTGGGAA	CCAAGATCCT
2151	GAAGCTTGTG	AGAACAGAGT	CCTGGAATAA	GCCCTGAGAT	TGCAGCACTC
2201	AGCAAACCTG	CTTTCCCTGAG	AGCCTACCAG	ATGCCCATGT	GAAAGGGGGG
2251	TGTCAGTTCC	ATCTTATCTA	TGAGTGACAG	AGGCTCCAGC	AAAGACACCA
2301	GTCACTGTTT	CTTGAGTAGT	GAAGCTGCAG	AGCTAAGTCT	CAGCCTCTGC
2351	CTTAGGTGGT	ACCCATTGGA	GAAAACAGAA	ATTGGGCCCC	TCCTAAGACA
2401	GGAGTTTCCT	AAATTGTTGA	GTGCCTTTTT	TGTTTCCCTAG	GCCTCAGTTT
2451	CCCTGTCTAT	CATCACAGAG	AATCAGGGCA	AAAGGTGTCC	CTTCTGTGGA
2501	CCCCAGAACC	TGATGTAGGT	CCAAGTCCTG	TTTATGCAC	ATGCCTTGAC
2551	CCTGGCAGCC	CTGGCGGTGG	TGCAGCATGG	GAAGTACAGG	GGATGAGGGC
2601	TAGTCATGGG	CCAGGGGGTC	TTTCTGAGGG	ATCTTGGCTG	TCTACCTTCC
2651	AGGAAAATAT	AATCAACACT	AATAAAGGAG	GAAGGAGAGC	AGCTGGGGTC
2701	TCACTTTGAG	GGAGGCTGGG	GACGTGACAG	TCAGACACCA	CCCTGAAGAG
2751	GCCACTCGCT	GGCTTCACCC	TCTGCATCTT	AAAGTTATTG	GGAAGGTTTG
2801	ATACACAGAG	GAGATCCATT	CTAATGGAGG	GTTTGATTAG	GGGACTAGAA
2851	TCAACAATAA	ATTCTAGAT	GAGGAAGTGT	TTATATCCAA	CTCTGAGAAC
2901	AGGTTAGGGT	TACATGGGAT	TGGAAGAGAG	GGTGGGGTCC	CTTAAAGAA
2951	AAGCCCCAGA	AACTCACTGC	TGCTCTATCC	CTCCCCTATA	AGTTCTCTTT
3001	GTTATCTTCC	ACCCAGGACC	TGTCAGAATC	CCACCCTTCC	TTCTGTCTCC
3051	CATCGAAGTC	CTCCAGGAAA	TGCAGCTGTT	TCAGTGACAG	GGGGTGATTG
3101	CCATCTTCCA	ACTGAGGAGG	AATTTGGGGT	TTTGGTCCAG	TCCATGAAGT

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3151	GTGACACAGT	CAGAATAAAA	GGTGAGGGCC	TAACAGATTA	GCAGACGGTA
3201	GGAGAAGACT	ATCTTGCAGC	CAGCTTCAGA	GAGCCTGTGG	CCATGGCTCC
3251	CAGGTCAACA	TTAGGCCCTG	TTGCCTGGGA	ACCCCTGGGC	AGGCAGTGGG
3301	AAGGTTGAGG	TGTGGCTCCT	GGTAGCCTCA	GAAGTCCAC	TATTTCTCTGA
3351	AGCTCCTACT	TGTTCTGTCA	GCTAAGCCCC	CATCCCAGTA	GGCCAGCAAC
3401	ACCCTCAAGA	CCAAGAACAG	GCCATGGTGA	ATCTCAGGGC	CACTAAGTAC
3451	CTGGGCTGGC	AGGGGCAGAG	TGCCTCAGGG	CTCAGTGTG	TTTGGGCTGA
3501	GCATGGGCTT	TGGGAGTCAG	ACAGCTGCAC	TGGGCTCCCA	GCTGCACCAT
3551	GGCCAGCCCT	GTGTATGGGG	CACTGCTCTG	TAAGTTGAGA	CACCATAGTC
3601	ATAAATATAA	CACACCCCTT	TAAGTGTCTT	TTCTTTTTTG	TCTATTTTTT
3651	TCTATAATCC	CCATGTACTA	CTGATCTGTT	TATTTAAATT	AATAAACATG
3701	TTATACAGTG	TATATGTTC	TTCTCATGA	TTTCTTTACT	ATATGTGTG
3751	ATTCCACTCA	TATGAGGTTT	TTATGGATGT	CCCATTCA	GAAACACAAA
3801	GTAGAAGAGT	AGTTAGTTCC	CAGGGGCCAA	AAGAAGGTAA	ATGGGGGCTG
3851	TTCTATCTTT	TTATTTTAT	TTTGCAAAA	TGAACAAAAT	TCCCTATGAA
3901	TGTGGATGAT	GGTTGCAGAA	CAATCTGAGC	ATGATTAATT	CCTCTGACTT
3951	GCACGTTAGA	AATTGTTAAA	ATAGTTAATT	TTATGTATAT	TTTACCACAA
4001	TGTAAAAAAG	GAATTTTAA	ATGAACAGAC	TGTAGATACA	TGCAACAGCA
4051	TAAATGAATA	TCACAAATAT	AATCTTGCAT	TTAAAAATTG	ATGTAAAAGT
4101	ATCCAACTA	TATAATTCA	TTTATACTAA	ATCCAAAAAT	CAAACTGAC
4151	ATTCTTGCTT	TCACTAATGG	GAATTAGCTA	GTTAAACTAA	CACTCTCAGA
4201	GAGAAAAATG	ATGAATCCTA	GATAAAATAG	TATATATCAT	TATAAACACT
4251	TCTATATATA	ATACATATAT	GAGATATGTG	TGTATAAGAA	GTGAATGAGG
4301	ATGTCCCCTG	TGCCCTCCTT	AGGAGAGACA	AGAATTGAAG	TTATAATCCA
4351	GGCCAATTAG	CACTCTCTTT	AAAAATCAAC	ACTCTTCAAA	GGGACACAAC
4401	AGAATCCAGA	GTCTCTATAA	CTCTGTATA	CAGTCTCTTG	TACACAATTT
4451	TCAAATTCGT	GAGATGGGTG	AAGACACATG	AAAATGCAAT	ACATACACAA
4501	GATAAAAGGC	AGGCAGTAGA	CATCTCCAAG	ATATCCAAGA	TGTAATCAGC
4551	AGACAAGAAT	TTGAAGGCAG	CTATTACAAG	TATGCTAATG	GAGGCAAAGG
4601	AAAAAATATA	CTTATAAAGG	AACAGATGTG	GAACCTCAGC	AGAGAAATAA
4651	AAAATAGCCA	AATAGAAAAA	TAAGACACAA	AAAGAATAAT	TTTGAGCTTA
4701	TCTATAGATC	AGAAACAAAA	CACACAACAA	TAGAAATTAT	TCAATCTGAA
4751	GATACAAGTA	AAAAAAAAG	TTTAAGGAAA	ATGAACCCAG	CCTTACAGAC
4801	CTCTCATGGG	GCACCTGGG	AGTTGTAGTC	TCTTCTCCG	TTCCAAACGG
4851	TGGCTGTTGT	GGCTGCAGGA	TAACAGTCCC	AGATTGAGAC	AGGGCAGAGG
4901	CTGTGTGCAG	CCCTACAGGA	AGGGGCAGGG	TGGTGTAGGC	CTCTTCACTT
4951	ACCAAGATTT	GCTGGCCATT	GATTCCGTGC	CAAACCCCTC	CCAAGGGGAT
5001	TGAGTCAGGA	GAGGATCTTG	AGAGTCACTC	AGGGTCTTCC	CAGAGCATCT
5051	GTGCCTCCTC	CAGCCCACGG	AGCTGCCTGA	TTTCCTAAGT	GGCTGTGGGA
5101	ACTGCTCTGA	AGTACCAGAC	GCTGTCTACT	GTGCTGCTGC	CCTCTGTTCT
5151	ATCTAACCAA	AGTGCAAGTT	CAGCTGCCTT	TGAAAGACAT	CCACTGCCTG
5201	ACCTGGGGAT	GCACGGGTTT	AGAGCTTTGC	AGGGAGTGAA	CATGGGCTGT
5251	GGCTTCATGA	AAATATCACC	CTCCCCAACG	CGTTTTTGCA	GATCTGGACT
5301	TGGAGGCACG	AAGGACGGTA	ATCATTGGGT	TACCAAGGTG	TTACTAGGAG
5351	CAGAGGAGAA	AACCGCAATT	CCTAGCCATG	TGTCTGGTGT	GACATTTTCG
5401	CAACCCATTT	AAGTGTGCAG	ACCCCAAAAT	ATCTACCTAA	AGATTATGAT
5451	AGTTTAGGCA	TTTTACATTT	AAAATTATTG	GCTTCATGTC	CACTGAAGCC
5501	TGACTGGCCA	GTGTCTCAA	GACACAGATG	ATGATCTGAT	CCCTCAGGAA
5551	CAGATGGTTC	TCCAGCTTTG	TTGGAGTGAC	TTTCAAGGTA	TGGAGCACTT
5601	ATATAAATTT	GCCTAAGAGT	AGGATTTGTG	CTAAGTACCT	GTTCACAATA
5651	ACATCAAGGT	TGTTTTGATT	TAAGGGTAGG	GCTTACATAA	GCAGTAGATT
5701	TCAATATATA	ACATAGATTC	TTGAAACCCC	CCCAAAAAAC	ATTAAAGGAA
5751	GTACCTATGT	CATAATTTTA	ATTTTTTATT	TAGTAATTTA	AAATCTTAAC
5801	GTCTTGTTTT	GTTAGCTAAT	CTTAAGTTTC	TCACTAAAAA	TTAGCATGAT
5851	TAAGCATGAA	AATAATAGCT	TTAAGACAGT	TTTTACCCCA	GAACCAGTGA
5901	TTGGATAATA	GGGTTCAGG	CCCTCCCCTT	CAGGTCCCTG	GTGACAGAAT
5951	GTGAACCAAT	TCATAGCCAA	GCGAGGAGAG	AGTGAAACGT	TCCTAGGTGC
6001	AGCCCCTTTC	AGGCAGGACT	TACTCCTTAT	GCTGAAACCT	GGCCCTCACT
6051	ATGAGACATT	TGCATTTAAC	CTTGATATATA	AGTTTATTTT	TATTCATAAA
6101	TTATATATAT	GCACATATAT	GTATATATAC	AGCTGGACAT	GGTGAATCTC
6151	ACCTGTAATC	CCAACACTTT	GGTAGGCTGA	GGGGCAGGGA	GCTCTGAAA
6201	CCAGGAGTTC	GAGACCAGCC	TTGGCAACAT	AGTGTGAGCA	CCCTCCGCCC
6251	CCCAACCTTT	TCTACAAAAA	AAAGAAAGAA	AGAAAAAATA	GCCAGGCATG

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6301	GTGGAGCTTG	TCTGTGGTCC	CAGCTACTTG	GGGACTTAG	GTGGGAGGGT
6351	CATTTAAGCC	TGGGAGGTAG	AGGCTGCAGT	GAGCTGAGAT	CAGGCCACTG
6401	CATGCACTCC	AGTCTGAGTG	ACAGAGCGAG	ATCCTCTCTC	TCTATCTCTT
6451	CCTCACTCTG	TGTGTGTGTG	TTGGGGAGAG	GGGTGTGTGT	TTGTGGGTGT
6501	GTGTGTGAGT	GTGTATGTGT	GTTTATTATT	CAAAATGAAA	ACAACATAAT
6551	GACAATTATT	TTTATTTTAA	TTTTTTTGAG	ACAGAGTCTC	ACTTTGTCAA
6601	CCAGGCTCCA	GTGCAGTGGT	GCGATCTCGG	ATCATTGCAA	CCTCCGACCC
6651	CGAGATTCAG	GCAATTCATC	TGCCTCAGCC	TCCTGAGCAG	CTGGGATTAC
6701	AGGTGCCCCAC	TACCTTGCCT	GGCTAATTTT	TGTATTTTAA	GAAGAGGCAG
6751	GGTTTTGCCA	TGTTCTCCAG	GCTGGTTTTG	AACTCCTGAG	CTCAAGTAAT
6801	CCGCCCCACCT	TGGCCTCCCA	ATGTGCTGGG	ATCACAGGCA	TGAGCTGCCA
6851	TGCTCGACCA	ATGACAATTA	TTTAAAAAAT	TTAGATTTTA	CAATCTTTCT
6901	GGCCTTTTGG	CTTTTGAGGC	AGCCTGAGCT	GTGAAAATAG	GCAATCCTCT
6951	ATTGCAGCAA	TGTGCAATAG	AAGTAAAATG	TGAGCCACGT	GTGTCAAATA
7001	AAATTTTGTG	GTAGCAACAT	AAAAAAAAGAA	AAATGAGTGA	AATTGATTTT
7051	AATAACAATA	TATCGGAAGT	ATTTTAACAT	ATGATCAGAA	TTAAATTATT
7101	TTATATATAT	ATTTTGGGAA	GCACACAATT	CAGCTCACAG	CAGCCTCTGT
7151	CAGGACATAA	CGTTTACATT	GAGATCCCAG	TAACCTAGCA	ACAGAGGGAA
7201	TGACATACAA	AGATTCTGGG	GAAGAAGATT	CCACACAGAT	GATTCTATTG
7251	AGCAATGGTC	CTGAAATGGG	AGTGAACAGG	GTGAGTTTAA	GGAACCAGAG
7301	ACCAGTGAAT	GCAAGGAAGA	GCTATGAAAA	GCAAGGAGAG	GAGGTGAAAT
7351	CACAGAGATC	CAGTGAGATA	TATAAACTTG	ATTGTGATTT	AAGCAGTTTC
7401	TACCTTTTGG	ATTTTGAGAA	CAATACTGTT	ATTAACATGA	GTGTGCCAAT
7451	GTTTCTTGCA	GGTCCTGCTT	TGAACATTTA	GATAGATATC	CAGAAATGAG
7501	ATTGCCAGAT	CGTATTAGAA	TTCCATTTTT	AGTATTCTGA	GGAATATCTG
7551	TACTATTTTT	CATAATGGCT	GCATTATTAT	TTTTTCCACC	ACCAAGTGTAC
7601	AGTGTTCCAA	TTTCTCTACA	TCCTTGAGAA	CATTTGTTAT	TATTCTTTGT
7651	TTGATAGTGG	CCATCCTAAT	GAGTGTGAGG	TAATATCTCA	TTGGGATTTT
7701	GCTTTTTTAT	TCTCTCAAGA	TTTGTAGTTT	TGAGCATCTT	TCAAATTCCT
7751	CTTGGCCATT	TGTATACTCG	GTTTTTAAAA	ACATACGTTG	ATCATTTTGC
7801	CCATTTTTTAA	ATAGGGTTAT	TTACTTTTTG	TTGTTGAGTT	TTAGAGGTTG
7851	TTTATACATT	CTGGATATTA	ACGTCATCA	AATATGTTAT	CTGCAATTTT
7901	TTCTCATTTG	TTAAATGACA	TTTTTACTCC	ACTTAATGTT	TTCTTTGATG
7951	AGTGAAGAGC	TTATTACACT	TGATGTAGTC	CCATTTTCTC	GTTTTTTATT
8001	TTGTTACTTC	TGCTTTTAAT	GTCATGTTCA	AAAAATTACC	AGGACAAATG
8051	TCACAATTGT	TTACCCTATA	ATTTATTTTA	AAAGTTTTAG	AGCTATCTTA
8101	CTTACATTTA	AGTATTTAAT	TCATTTAAGA	TATTTTTTGA	TACAGTGCAA
8151	GTGAAAAGTT	AAATTTTCATT	TTTTTTAATT	TTGATATTCG	GTTTTGTAAAC
8201	ACTATTTGCT	AAAGCGTCTG	TTCTTCCCCT	TTGTTCCGTC	ATGGCAACTT
8251	GATTGAAGAT	TATTTGCTGA	TATTCATGAA	GATTTATTTC	TGGGTCTCTC
8301	ATTCTGTTTC	ATCATCTATT	TGTCTTCTG	TTTGAATTTT	TACAGCTTTG
8351	TAATATATTT	TGCAATAAAG	TTGCAATCCA	ACTTTGTTCT	TCCCTACAGC
8401	TATTTTGGCT	ACTCATGTGC	CCTTGAGATC	CCATATGCAT	TTTAGGACTT
8451	AAAATAATAT	TTCTCCAAAA	AAGAAAATCT	AGCTTTTGTG	CCAGACATGC
8501	CTTGAGATTC	CATATAAATT	TTAGGACTTA	AAATAATATT	TCTCCAAAAA
8551	AGTAACATTG	AGATTTTGAT	ATAAAATACT	TTTCTTTGAA	TTTGTGCTTC
8601	AATCCAAGTA	GTATTGACAT	CTTAACAATA	ATAAAATTTT	TGATCCTTGA
8651	ACAAGAGGTC	AAGAGTGTGC	TGTTTAAAGT	TTCATATATA	TTTTGATTTG
8701	CCAGTTTCCT	TCTGCTTGTG	ATTTGTAGAT	GAGGGCTTAT	TATGTTGCCC
8751	AGGCTGGTCT	CCAACTTTTC	GCCTCAAGCT	ATTCTCCGTC	ATCAGCCTCC
8801	TGATGTATTT	GGATTACATA	GATAAGCCAC	TGCACCTGGC	CTCTTTATTG
8851	TTTTTCTTAC	ATTTTATGTA	TTTGAAGGTA	ATTTTGTGAA	AGATTTAAAA
8901	ATATGTATCT	CCTTAGAAGG	TTTTTCATTT	TAATGTAGTC	AAAAACACGT
8951	AAAATTGACC	ATCTTAAATA	TTTTAAGTAC	ATAATTAAAT	AATATTAAAT
9001	ATATTTGCAC	TGTCATGCAA	CATATCTCTA	GAATGTTTTT	GCTGCAAAAC
9051	TGAAACTCAA	TATCTATGAA	ACAACAATA	CCCCTTTATC	TCCTCCCCTG
9101	AGGCTCTGAC	TACTTTCTGT	TTCTAGGAGT	TTAACTACTT	TAGATATCTT
9151	ATTTAACTGG	AATCACACAG	TGTCCTTTTG	TGGCTGGTTT	ATTTTATTTA
9201	CATAATGTCC	TCAAGATTTA	TGTTTAGTGT	AAAAATAATC	AGATCTCCTG
9251	CTTTTAAAAA	ACTGAATAAT	ATTCCATTGT	TTGTATATTT	CAAATTGTCT
9301	TTACCTACTC	AATCACTGAG	GGACGTTTGG	GCTGCTTCCA	CCTATTAGCT
9351	TTTGTGAGCA	ATGCTGCAAT	GCATATGGAT	ATACAAATAA	TTCTTCATTT
9401	GGCCATATAT	ATGAGATTTT	ATTTCTGTGC	TCTGTTCTTT	TCCGTTGGTC

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9451 TGTCTGTCTG CCTTTATGCC AGTACCAAT GGTGGTTA CTGTAGCTTT
9501 GTAATACATT ATAAAGTCAA GGAGTGTGAT GCCTCCAATA GCATTTCTTT
9551 CTTTGAAGTT TGTGGTTTC TCGATACTCA CTTTAGATT CATATAAGTT
9601 TTAGAATTTT TTTTGTATT TCTTCAAAAT AATATGACAG TTAATAAAG
9651 ATGGAGATGG CATTAAATCT GTAGATCACT GTGTAATGTG GACATCTTCA
9701 CAATATTGTC TTCCAACCTT TGAATAAGAG CATGCTCAAA AGTATGTTGT
9751 PTAATTTCCA CATGTTTGT GATTTTGCAG TATTTTCTG CTATCAATTT
9801 CTAATTTTAT TCCCTTTTAA TAAAAATAA TAGTTTGTAA TATTTAATC
9851 TTATTTTGTG TATGTTGTAT GTTGACACCC TAAACCCAG TACGTAAGAG
9901 TGTGGCTATA TTTGAAGAAA GTGTCATCAC ACAGATAATT ATGTTAAAT
9951 GAGGTCCTTG GGGGCACAGG TGGGGTGGTG GAGAGAAGGT CACATTATAC
10001 AAAATTTTCAG TTAGGAAGAA TAAGTGCAAG AGATCTATTG TACTTGGTGA
10051 CTACAGTTAA TGTATTGTGT TCTTGACTAA TACAGTAGAT TTCGAGTGT
10101 CTCACAACAA AAACATGATG GGTATGTGAG GTAATGCATA TGCAAACTAG
10151 CTGGGTTTAA CCATTCCACA ATATGTGTGT ATTTCAAAAC AGTACCATAA
10201 ATGCAGACAA TTTTGTGTCA GTTACAATCA AAAAAGTTT AAAATGAGGA
10251 CCTAGGGTG GGTCTAATC CAATCTAAGT GATGCTCCA TGAAAGAGGA
10301 AATAAGGATA CAAATGTGCA CACAGAGAGA AATGGCCACA TGAGGACACA
10351 ATGAGAATGT GGCTACTTAC AAGCCTAGGA GAGAGGCTC CGAGAAAACA
10401 CACCCTACCC ACACCTTGAT GTTGGACTTC ATCCTGTAGA CGAAGTCCTC
10451 CACCTGCTT CATCAGGTGG AAGCCTTTGA TTCTGAATAT TCTCCAAATG
10501 CTGGAAGGTA CAAAAGTGAA GAGACAGCAC AGACCTCAGG GTGAAAAGTT
10551 TAAAGAGAAT AACATCTTTC CATTGCTGTG TCCTATCCCC TACACACACC
10601 TATTCCAGTC TTTATTGGTC TTTTGTGTTT TCGTGTCTG GGTATAGTGT
10651 TAGTTGTAAT TCTGTGTTTA CATACAGGAT AACATAAAAC AAAGGTAAAC
10701 AATAAAATAA AAACAGACAG CAAAACCTCA CTAATAGTGT TTGGGCATGG
10751 TGACAGTGAA GACAGGAGAG TCACATAAAA ATGGAGGTGG AACTTTTGAG
10801 CTAATCAAT TCTGTGAGTA GTTCTGTGT TTCTACATCA GACTCTATAG
10851 TGGCAATTGT CAGGTAGGT GTTTTATCC TTGCCTGCTC AGTAAGTGCC
10901 AGAGGAGATT TTTCTAACT GGGTGAGGAA CAGGTAGAGA AGTGAAGTG
10951 AGACAACTT CCCTGCCATT TGCCAAAGTG GCAGCACATA ATGTATCATG
11001 AGTGCCTCTA CCCTCTGATA TCCAAATAT CAACTCTATA GATGATGTTT
11051 TGTTGGCTCC TAATTTAGAA GCATCTGCCT TCATACTCTT TCCTAGAATG
11101 GTAACATCTC TCTGTGAGTA GCTGATAAAA TTAATAAAAT CTCATAGTTC
11151 TGTTTTCCAG TTAAGGTTCA CTGCAACTAT ATGGGCAGAT TTACATAGCT
11201 CAATTCTTCC AGCTTGACAT TGTTTTCTTT TGAAGCTTCT GAGAGAGGGA
11251 GTCAGCCTCC ACCTAGAGGT GGCCCTTGGA GTTTTGTACA CAGAATCTCC
11301 CTGACACTAC TACTTACACT GATTTGAAAG TCAGTGTTGA GGTGGCTTG
11351 CTACAATGCT CTTGTCAAAC TGAATCCTGC CACATCAAGG GCTTGGGCT
11401 TCCAGCTTA ATTTTCCAAT TTTGAAGTGA GAGAATTGA GTTCTACAAG
11451 ACATCAGAAG ACCGCTTAGA ATATAACACA TTCTAAAAGT AAATCGGAAT
11501 GCCACAGGAA CATCTAGTGT GTAAAAGAAA AATTAGGTTT TTTGGTAAAA
11551 ATTTTATGCC CCTTGATATG GTTTGCTGT GTCCCCACCC AAATGTCATC
11601 TCAAGTTTTA GCTCCCATAA TTCCCAAGTG TTGTGGGAGG GACCCAGTAG
11651 GAGATAATTG AATCATGGGA GTGGGTTTCC CCATACTGTT TTCGTGGTAG
11701 TGAATGAGTC TCATGAGATC TGATGGTTTC ATAAGGAGAA ACCCTTTGCT
11751 TTTACTCTCA TTCTCTCTTT TCTGTGTTGC CACCAAGTGA GACATGGCTT
11801 TTACCTTCTG CGATGATTGT GAGGCCCCCT CAGCCATGTG GAACTGTAAG
11851 TCCATTAAAC CTCTTCTTT TGTAAATTT TCAATCTGA GTATGCTTT
11901 ATCAGCAGTG TGAATGAA TGAATACACC TCCCTTCACT GTTTGAAGAA
11951 AAAGTCTGG CTCTATGAGG TCTTCAGTTC ACTGAATATT TTTAAATGC
12001 CTAGCCCTAA CTCACAGACA AGTCAAGGAA GCTGCCACCT TATGGTGTTC
12051 ACTAGGCTAC TGTGGATAGC CCTCATTGCC AGGCACACAG AACCTGAAGC
12101 AGGGGTGGCT GCTCCACTTA ATGGTGAGAG CTCAGGGTTT TGGGTCATTG
12151 TACATGTTCT AACTGTTTGG TCTCCACAT TGAAATTTAA GGCTATTAGA
12201 TTAAGGACAT CCTTTTTCAG ATTCAAATCA TGCAGAAAT CAGCTGCTGA
12251 TCTGTAAGGT CATTCAATTA AGAGTCCATG GTAAGGGTTG GTCCTCCGAA
12301 AATGCTAACC ACAGTTAAGC CAAAAACCAA GCCTGAACCC ATGTGTAATG
12351 CAGTGGTCAT CACTGCATGC CAGATTTGTT CTCCTGGTG AAAGTTGACC
12401 TATTTGTCTC ATGGTTTAGA AGGCCCCAGA CCATTCTTGG CATAATAACT
12451 GCATTGGCCT TTGGCCACT TCCTGAAGTG TTGGTCATGT CTCACCACTA
12501 TTAACACTTT TAGGATAATA ATCAGCTGAC TCCAGCCAAA GCATGTGTCC
12551 CTTGAAGCTC ATTCATGTAA TATTTTAGGC TTTTGAGACC AATTGCACTT

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12601	AAATCACATT	GTAAC TTTTA	TCAC TAAATC	TGTTAACATG	GCCAAACTGT
12651	TTGATTTTAC	TTCCTTTTTT	CCTTTAGGTT	CACACATGTT	GGCTACGTAA
12701	TTTGTGATT	GAATGTGACT	GTCCCCCAG	CACCCAAAAA	TCTCTTCTTG
12751	ACTGACTCCA	AGATGAAGAG	AACATCATTG	AGTTCTATAG	GCATCCATTT
12801	TCAAAATTTG	ATATTTCTCA	CTGACCTTTC	CTGGACAGGA	TGTGTCTTTC
12851	TTTTCTTAAG	CTGCAACCCC	AGGCAAATCT	TGTTTGTTACA	TTCTCTGAAT
12901	GGCAGTCCAA	CCCAAAGTGG	GGTTGTGGTT	TTCAACTTAG	TTGTGGTGAA
12951	CATTTACATA	GTTCTTGCAT	CCATATCATC	TGGCTCTACT	AGAAAAAAA
13001	ATTACTAGAA	GACAGTATGG	GTGACTAGAA	TAGAAAAAAT	GACTACTTAA
13051	AATTATAGGT	ACTGGCATAG	CACACATAAA	TTCTGTGGCT	GTAGAGGAAA
13101	GACAAAACCC	CAAAACCTAA	AAGTGAACAA	ATTAGACCCA	GGAAC TACAG
13151	AAAAGGAGGG	AAGTTAATAT	CTTTCTGTCT	TTCTGAATTA	TCCCTAGTGT
13201	GGCCCAGAGA	AGAGTTGGGG	AGTCCTGTTG	GGCCAGAATG	AGTAGTAGTA
13251	TTAGTTAGAC	CAATGGTAG	AACAGGATGG	GTGGGTTTCA	TTTCTCTAAG
13301	GAATTTTCATC	CTTTTGTGAT	GTAGACATGG	AATCCCAGTG	AGCATCCTGC
13351	ACTCTCAGTG	TCCAAC TGC	TGAAACCACA	GTTGTTTCTG	AAGACTGAGA
13401	ACAATTGCTT	TTTGCTGAGG	AGACAGCACT	CCACAGCTGA	GGTAAGGTGG
13451	ATTCTATAGA	GCATTAATTC	CATTTTCTCC	TTCTTCTGTG	AGCTGGGTTT
13501	CTTTCTTCAG	TTTTTTATCT	AGAGATGAAA	TTACATTGTC	AATATTTGTG
13551	TAAAATAGAG	ATATAAGTCT	GGCAAGTAGA	CGCTTAGATG	CAACCCCTCAG
13601	CAGAAATTCT	GGTCTGTTTT	TCTTCTCACT	TTTATTCAAT	TTTTGT CACA
13651	GAAAGATGCC	CTGACATGTG	GTCTCTCAAG	AGTGATTAGA	ACATTGTACT
13701	TCTAGAGGAG	TTAGTTGATG	GAACATGGCA	GAGCTTAGAA	TGAGGATGGA
13751	AGCCTCTGTC	CAAATCTCCC	AGGCTATCTA	TGTGTGGGAA	GTGGAGTCAG
13801	GAAAGACCTT	AGAGCTTTGG	AAGTGATCAT	TAAGAGAAAA	CAAAATCCCT
13851	GTAAATTAGA	GTACAAGGGA	ACATATTCAT	TAGCCACCTT	TAGAGTCAGA
13901	TGCTCAGGGC	TGAGCTGGTG	TGGGGGAGTG	TT CAGACCTG	TGCATGCCTG
13951	GGAAAGCCTC	CGATCATGTA	TGAATGGTGA	GGCTTCTGGG	TGCATGAGAT
14001	TGAGTGCCCT	TCCTTGGCAG	AGCACCACTG	AGTGAACAAT	TGATTTAGGA
14051	TCAAGCATAT	GGAGATCAAC	TTTATTTTGA	ATATCTCAAA	GACAGAAACT
14101	GAAAAGATTT	TTTTTGCACTT	TGAAATTGAG	TAAGGGTGTC	AGAAACTTCA
14151	GTAAAAAAGT	CACAGGAGGA	AACCCAGAAG	TCTTATTCAT	CCCCAGAAAC
14201	CACCAAAATC	CTGATCCAAA	CTGTAAAGAT	TCACCTCGTA	AAAAATTTGAT
14251	TTTTGAATAG	GAACAGCTCC	GGTCTACAGC	TCCCAGTGTG	AGCGATGCAG
14301	AAGACGGTTG	ATTTCTGCAT	TTCCATCTGA	GGTACCAGGT	TCATCTCACT
14351	ATGGAGTGCC	AGACAGTGGG	CGCACGTCAG	TGGGTGTGCG	CACCGTGCGC
14401	GAGTGAAGCA	CGGTGAGGCA	TTGCCTCACT	CACGAAGTGC	AAGAGGTCAG
14451	GGAGTTCCCT	TTCTTATTC A	AAGAAAGGCA	TGACAGATGG	CACCTGGA AA
14501	ATCGGATCAC	TCCCACCCGA	ATACTGCGCT	TTTCCGACGG	GCTTAAAAAA
14551	TGGTGCACCA	GGAGATTATA	TCCTGCACAT	GGCTTATAGG	GTCTTACGCC
14601	CACAAAAGTCT	CAC TGAATTGC	TAGCACAGCA	GTCTGAGATC	AAACTGCAAG
14651	GTGGCAGCGA	GGCTGGGGGA	GGGGCGCCCG	CCATTGCCCC	GGCTTGCTTA
14701	TGTAAACAAA	GCAGCCGGGA	AGCTCGAACT	GGGGTGGAGC	CCACCATAGC
14751	TCCAGGAGGC	CTGCCTCTGT	AGGCTCCACC	TCTAGGGGCA	GGGCACAGAC
14801	AAACAAAAAG	ACAGCAGTAA	CCTCTGCAGA	CTTAAATGTC	CCTGTCTGAC
14851	AGCTTTGAAG	AGAGAAGTGG	TTCTCCCAGC	AAGCAGCTGG	AGATCTGAGA
14901	ACAGGCAGAC	TGCCTCCTCA	AGTGGGTCCC	TGACCCCTGA	CTCCCGAGCA
14951	GCCTAACTGG	GAGGCACCCC	CGAGCAGGGG	CAGCCTAACA	CTTCACACAG
15001	CTGGGTACTC	CAACAGACCT	GCAGCTGAGG	GTCTGTCTG	TTAGAAGGAA
15051	AACTAACAAA	CAGAAAGGAC	ATCCACAACA	AAAACCCATC	TGTACATCAC
15101	CATCATCAAA	GACCAAAAGT	AGATAAAACC	ACAAAGATGG	GGAAAAAACA
15151	GAGCAGAAAA	ACTGGAAACT	CTAAACAGCA	GAGTGCTCT	CCTCTCCAA
15201	AGGAACGCAG	TTCTTCACCA	GCAATGGAAC	AAAGCTGGAC	AGAGAATGAC
15251	TTTGACAAGC	TGAGAGAAGA	AGGCTTCAGG	TGATCAAATT	ACTCCAAGCT
15301	ACGGGAGGAT	ATTCAAACCA	AAGGCAAAGA	AGTTGAAAAC	TTTGAAAAAA
15351	ATTTCTGAAGA	ATGTATAACT	AGAATAACCA	ATACAGAGAA	GTGCTTAAAG
15401	GAGCTGATGG	AGCTGAAAAC	CAAGGCTAGA	GAAC TACGTG	AAGAATGCAG
15451	AAGCCTCAGG	AGCCGATGCG	ATCAACCGGA	AGAAAGGGTA	TCAGCGATGG
15501	AAGATGAAAT	GAATGAAATG	AAGCGAGAAG	GGAAGTTTAG	AGAAAACAGA
15551	ATAAAAAGAA	ATGAGCAAAG	CCTCCAAGAA	ATATGGGACT	ATGTGAAAAG
15601	AGCAAATCTA	CGTCTGATTG	ATGTACCCGA	AAGTGACGGG	GAGAATGGAA
15651	CCAAGTTGGA	AAACACTCTG	CAGGATATTA	TCCAGGAGAA	CTTCCCCAAT
15701	CTAGCAAGGC	AGGCCAACAT	TCAGATTCAG	GAAATACAGA	GAATGCCACA

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15751 AAGATACTCC TTGAGAAGAG CAACTCCAAG ACACATAATT GTCAGATTCA
15801 CCAAAGTGGG AATGAAGGAA AAAATGTTAA GGGCAGCCAG AGAGAAAAGC
15851 CAGGTTACAC TCAAAGGGAA GCCCATCAGA CTAACAGCAG ATCTCTCGGC
15901 AGAAACTCTA CAAGCCAGAA GAGAGTGGGG GCCAATATTC AACATTATTA
15951 AAGAAAAGAA TTTTCAGCCC AGAATTTTCAT ATCCAGCCAA ACTAAGCTTC
16001 ATAAGTGAAG GAGAAATAAA ATACTTTACA GACAAGCAA TTCTGAGAGA
16051 TTTTGTCAAC ACCAGGCCTG CCCTAAAAGA GCTCCTGAAG GAAGCGCTAA
16101 ACATGGAAAG GAACAACCAT TACCAGCCAC TGCAAAATCA TGCCAAAATG
16151 TAAAGACGAT CGAGACTAGG AAGAAACTGC ATCAACTAAT GAGCAAAATA
16201 ACCAGCTAAC ATCAAAATGA CAGGATCAAA TTCACACATA ACAATATTAA
16251 CTTTAAATGT AAATGGACTA AATGCTCCAA TTAAAAGACA CAGACTGGCA
16301 AATTGGATAA AGAGTCAAGA CCCATCAGTG TGCTGTATTC AGGAAACCCA
16351 TCTCACGTGC AGAGACACAC ATAGGCTCAA AATAAAAGGA TGGAGGAAGA
16401 TCTACCAAGC AAATGGAAAA CAAAAAAGG CAGGGGTGC AATCCTAGTC
16451 TCTGATAAAA CAGACTTTAA ACCAACAAAG ATCAAAAGAG ACAAGAAGG
16501 CCATTACATA ATGGTAAAGG GATCAATTCA ACAAGAAGAG CTAATATCC
16551 TAAATATATA TGCACCCAAT ACAGGAGCAC CCAGATTAT AAAGCAAATT
16601 CTTAGTGACC TACAAAGAGA CTTAGACTCC CACACAATA TAATGGGAGA
16651 CTTTAAACACC CCACTGTCAA CATTAGACAG ATCAACGAGA CAGAAAGTTA
16701 ACAAGGATAC CCAGAAATG AACTCAGCTC TGCACCAAGC AGACCTAATA
16751 GACATCTACA GAACTCTCCA CCCCAAATCA ACAGAATATA CATT'TTTTTC
16801 AGCACACAC CACACCTATT CCAAAATTGA CCACATACTT GGAAGTAAAG
16851 CTCTCCTCAG CAAATGTAAA AGAACAGAAA TTATAACAAC CTGTCTCTCA
16901 GACCACAGTG CAATCAAAT AGAACTCAGG ATTAAGAATC TCACTCGAAA
16951 CCGCTCAACT ACATGGAAAC TGAACAACCT GCTCCTGAAT GACTACTGCG
17001 TACAAAACGA AATGAAGGCA GAAATAAAGA TGTTCTTTGA AACCAACGAG
17051 AACAAAGACA CAACATACCA GAATCTCTGG GACGCATTCA AACCTGTGTG
17101 TAGAGGGAAA TTTATAGCAC TAAATGCCCA CAAGAGAAAC AGGAAAGATC
17151 CAAGATTGAC ACCCTAACAT TACAATTAAA AGAAGTAGAA AAGCAAGAGC
17201 AAACACATTC AAAAGCTAGC AGAAGGCAAG AAATAACTAA AATCAGAGCA
17251 GAACTGAAGG AAATAGAGAC ACAAAAACCT CTTCAAAAAA TTAACGAATC
17301 CAGGAGCTGG TTTTTTGAAA GGATCAACAA AATTGATAGA CTGCTAGCAA
17351 AACTATTAAA TAAGAAAAGA GAGAAGAATC AAATAAACGC AATAAAAAAT
17401 GATAAAGGTG ATATCACCAC TGATCCACA GAAATACAAT CTACCATCAG
17451 AGAATACTAC AAACACCTCT ACACAAATAA ACTAGAAAAT CTAGAAGAAA
17501 TGGATAAATT CCTCGACATA TACACTCTCC CAAGACTAAA CCAGGAAGAA
17551 GTTGAATCTC TGAATAGACC AATAACTGGA GCTGAAATTG TGGCAATAAT
17601 CAATAGCTTC AACCAAAAAG AGTCCAGGAC CAGATGGATT CACAGCCGAA
17651 TTCTACCAGA GGTACAAGGA GGAAATGGTA CCATTCTTTC TGAAACTATT
17701 CCAATCAATA GAAAAAGAGG GAATCCTTCC TAACTCATTT TATGAGGCCA
17751 GCATCATCCT GATACCAAAA CTGGGCAGAG ACACAACAAA AAAAGAGAAT
17801 TTTAGACCAA TATCCTTGAT GAACATTGAT GCACAAATCC TCAATAAAAT
17851 ACTGGCAAAC CGAATCCAGC AGCACATCAG AAAGATTATC CACCATTAGC
17901 AAGTGGGCTT CACCCATGGG ATGCAAGGCA GGTTCATAT ATGCAAAATCA
17951 ATAAATGTAA TCCAGCATAT AAACAGAACC AAAGACAAAA ACCACATCCT
18001 TATCTCAATA GATGCAGAAA AGGCCTTTGA CAAATTTCAA CAACCTTCA
18051 TGCTAAAAAA TCTCAATAAA TTAGGTATTG GTGGGATGTA TCTCAAAATA
18101 ATAAGAGCTA TCTATGACAA ACCCACAGCC AATATCTTAC TGAATGGGCA
18151 AAAATTGGAA GCATTCCCTT TGAAAACGGG CACAAGACAG GGATGCCCTC
18201 TCTCACCCTT CCTATTCAAC ATAGTGTGG AAGTCTGGC CAGGGCAATT
18251 AGGCAGGAGA AGGAAATAAA GGGTATTCAA TTAGGAAAAG AGGAAGTCAA
18301 ATTGTCCCTG TTTGCAGACG ACATGATTGT ATATCTAGAA AACCCATTG
18351 TCTCAGCCCA AAATCTCCTT AAGCTTATAA GCAACTTCAG CAAAGTCTCA
18401 GGATACAAAA TCAATGTACA AAAATCACAA GCATTCTTAG ACACCAATAA
18451 CAGACAAACA GAGAGCCAAA TCATGAGTGA ACTCCCATT CACAATTGCTT
18501 CAAAGAGAAT CAAATACCTA GGAATCCAAC TTACAAGGGA TGGGAAGGAC
18551 CTCTTCAAGG AGAACTACAA ACCACTGCTC AAGGAAATAA TAGAGGTTAA
18601 ATGGAAGAAC ATTCCATGCT CATGGGTAGG AAGAATCAAT ATCTTGAAAA
18651 TGCCCATACT GCGCAAGGTA ATTTACAGAT TCAATGCCAT CCCCATCAAG
18701 CTACCAATGA CTCTTTCACA GAATTGGAAA AAATACTTTT AAAGTGCATA
18751 TGGAACCAAA AAAGAGCCCG CATCGCCAAG TCAATCTTAA GCCAAAAGAA
18801 CAAAGCTGGA GGCATCATGC TACCTGACTT CAACTATAC CACAAGGCTA
18851 CAGTAACCAA AACAGCATGG TACTGGTACC AAAACAGAGA TATAGATCAA

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18901	TGGAACAGAA	CAGAGCCCTC	AGAAATAACG	CTGCATATCT	ACAACTATGT
18951	GATCTTTGAC	AAACCTGAGA	AAAACAAGCA	ATGGGGAAAG	GATTCCTTAT
19001	TTAATAAATG	GTGCTGGGAA	AACTGGCTAG	CCATATGTAG	AAAGCTGAAA
19051	CTGGATCCCT	TCCTCACACC	TTATACAAAA	ATTAATTCAA	GATGAATTAA
19101	AGACTTAAAC	GTTAGACCTA	AAACCATAAA	AACCCTAGAA	GAACACCTAG
19151	GCATTACCAT	TCAGGACATA	GACATGGACA	AGGACTTCAT	GTCTAAAACA
19201	CCAAAAACAA	TGGCAACGAA	AGCCAAAATT	GACAAATGAG	ATCTAATTAA
19251	ACTAAAGAGC	TTCTGCACAG	CAAAAGAAAC	TACCATCAGA	GTGAACAGGC
19301	AACCTACAAA	ATGGGAGAAA	ATTTTCGCAA	CCTACTCATC	TGACAAAGGG
19351	CTAATATCCA	GAATCTACAA	TGAACGCAAA	CAAATTTAGA	AGAAAAAAC
19401	GAACAACCCC	ATCAAAAAGT	GGGCGAAGGA	TATGAACAGA	CACTTCTCAA
19451	AAGAAGACAT	TTATGCAGCC	AAAAAACACA	TGAAAAATG	CTCACCATCA
19501	CTGGCCATCA	GAGGAATGCA	AATCAAAACC	ACAATGAGAT	ACCATATGAC
19551	ACCAGTTAGA	ATGGCAATCA	TTAAAAAGTC	AGGAAACAAC	AGGTGCTGGA
19601	GAGGATGTGG	AGAAATAGGA	ACATTTTTTAC	ACTGTTGGTG	GGACTGTAAA
19651	CTAGTTCAAC	CATTGTGGAA	GTCAGTGTGG	CGATTCCTCA	GGGATCTAGA
19701	ACTAGAAATA	CCATTTGACC	CAGCCATCCC	ATTACTGGGT	ATATACCCAA
19751	AGGACTATAA	ATCATGTCTG	TATAAAGACA	CATGCACACG	TATGTTTATT
19801	GCGGCATTAT	TCACAATAGC	AAAGACTTGG	AACCAACCCA	AATGTCCAAC
19851	AATGATAGAC	TGGATTAAGA	AAATGTGGCA	CATATAACCC	ATGGAATACT
19901	ATGCAGCCAT	AAAAATGAT	GAGTTCATGT	CCTTTGTAGG	GACATGGATG
19951	AAATTGGAAA	TCATCATTTCT	CAGTAAACTA	TCGCAAGAAC	AAAAAACCAA
20001	ACACTGCATA	TTCTCACTCA	TAGGTGGGAA	TTGAACAATG	AGAACACATG
20051	GACACAGGAA	GGGGAACATC	ACACTCTGGG	GACTGTTGTG	GGGTGGGGGG
20101	AGGGGGGAGG	GATAGCATTG	GGAGATATAC	CTAATGCTAG	ATGACGAGTT
20151	AGTGGGTGCA	GCGCACACAG	ATGGCACATG	TATACATATG	TAACCTAACCT
20201	GCACATTGTG	CACATGTACC	CTAAAACTTA	AAGTATAATA	ATAATAAATA
20251	AATAAATTTA	TAAAAAGAAA	ATTGTTGTTT	AAAAAAGTA	AAAAAATTG
20301	ATTTTTTTTCA	CCATATAGAT	TTATCTTTCA	TTTGACCTTT	ATTTAATTAC
20351	AAGTTTTTAGT	TAATACATTT	TATTTTACCT	TTATGATAGA	AATATCAGAT
20401	TCTTAAACTC	AAAGCATTA	TGATGCCTAC	CCAAGTGTAG	TTTTTATTGC
20451	CAATTAACTT	TCTACTATGA	TGCAAATTTG	TGTGTCTTTC	TAAAAACTCA
20501	TTTGTAAAAA	TTTAGTCCCT	GATGTGATAG	TTTAAAAACA	TGTAGCCTTT
20551	TTGGAAGTGA	CTAACTCAGG	AGGGCTTCAT	CCTCATGAAT	GTAATTAATA
20601	CCCTGTAATA	GAGGTGGAAG	GGAGCACCTT	TGTCCCTTCT	GCCATTGAAG
20651	ACACAGCAAC	AAGGCATCAT	TTATGAGAAA	TGGGACCCTC	CCCAGACACT
20701	AAATTTGCTG	GTGCTTTGAT	CTTGAACCTT	CCAGCTTCCA	GAAGTGTGAC
20751	CAACGCATT	CTGTTATTTA	TACATGACCC	AGTCTAATGT	ATTTTGTTTT
20801	AGCAATCTGA	ACAAATGAAG	ACACTTTCTG	ATGCACTGTG	GTTTATTTTT
20851	GAATTTATAG	TTCCACTGAG	CTATCTATAT	ATTCAAAAAT	CAACATGTCT
20901	CACAGGGTGG	GACAGCCACT	CTAATTATTT	TTTCAGAGTT	TTCTTAGCTG
20951	TTCTTATTTG	TGTTTTTCATC	TATAGGAGTT	CTCCAATACA	ATGCCTGCTT
21001	CCACTACCAA	ATGGTATCTA	TATTGGGACA	AAATTAAATT	TATTAATTAC
21051	TGCTAAAAAA	ATTGATGATT	GAGTAATAAT	GAGTTTTTCT	GCTTTAGAAC
21101	ATGATGTGAT	TTTCTATTTG	TTTATGCTGA	CTTTCCTATA	TTTCGAAGAC
21151	TTTTTATGTT	CTTTGTCTATA	CATTTTACAA	ATTCTTGTTA	GATCTATGTA
21201	TAGCTAGTTC	ATTTTATTTT	GTCCTGTTGA	AAAGTAAACT	GTAGCACAAT
21251	ACAAATTATA	CAAGTTTTTCT	TGGCAGGGAA	TGATGATGCA	TATCTGTGGT
21301	TCCAGCACTT	TGAGAGGCCA	AAGTGAGAGG	ACTACTTGAC	AAGCCAAAGT
21351	GAGAGGGGTT	GAGGCCAGCC	TGGGAAACAT	AGTAAGACCC	TGGCTCTACA
21401	AAACAGAAGA	AGAAATTAGC	TGGGTACAGT	GGTGCATGCC	TGTATTTCCA
21451	GCTACTCATG	AGGCTAAGGC	AGGAGGATGG	CTTAAGCTCA	GGATGTAAGG
21501	CTGCAGAGAG	CTTTGATTCT	ATCTATGCAC	TCTAGCACGG	GCGACAGAGC
21551	AAGAACCTGT	TTCAAAAAAC	ATTTTTTTCT	TGAGTAACAA	GCAACTAATG
21601	AATTGTGGAA	CACCGGACCA	AAAGAGGTTT	ACCATTTTAG	TGGCAAAGTG
21651	TCAGAGGTAT	TGAAGAAATG	CGGGAGCAAA	ATATTAAAT	TATTTGATTTC
21701	ATTGCAGGTA	TAAAATTGTC	TTATTTGGTT	TACCTTATAG	ACATATATTA
21751	CTATAAGCTT	TTTGAGTATT	TCTGATAACT	TAAGCTTAAA	TTCTGTTGTT
21801	GTTGTTTTTC	TAATACAGGC	ATTCACAAAA	AATAGCTCGC	ATTATGTTTT
21851	GCTTCTTTTG	AAATCAACAA	GATGATGTCA	CTGGGGAGGT	CTAACTGATT
21901	CTGTCTGCTC	AGGAATGTTT	CCAAGGCTTG	GTCTCCTTTT	TAATTTACTT
21951	TATAAATCAT	TTTGTAATTT	TTATCTCCCA	CACATTCTGT	ATCTTGTTAA
22001	TTACTTTTAT	ACATATGTAA	ATATATTTTA	TGTATGATTT	CTAAGTATAT

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22051 CACTCATGAA AATTGACTGT GACACAGGCA TACCTTATCT TATAGCACCT
22101 TATTGTGCTT CACAGATGTT GGATTTCTTA CAAATTGAAG GGTTTTGGCA
22151 ACCCTATATT GAATGACTCT ATTAATACTA TTTTCCAAC ATCATGTCAT
22201 CTTTGTGTGT GTGTATACCT CTGTCAGCAT TTTTTCAGCA TAAAGTACAT
22251 TTTTATTATA GGTATGTATA TTTTAAATAT AAACATGGGC TATTTCAATT
22301 TTATTCTACA GTATAGTGTA AACATAACTT TTATATGTTT TGGGAAGCAA
22351 GAAAAATTGT GTGACTCACA TTATTGCAAT ATTTGTTTTA TTGCACTGGT
22401 CTAGAGCAAA ACCCATATAT CTCAAAGGTA CATCTATATA TTTTATTGA
22451 ATTGGCCCCA TTAAGTAAA CGATAAATTG CTATTTCTTG ACTAAACAAG
22501 AGCTGTGGAG TGTGGAGAGG TCAGTGTGAA AATGAAGTAG AAGTGAATAT
22551 AAACAGTCTT CTAAGTACCA CAGGTAGTAA TACAAATTAA TTATGGATGA
22601 AATATAAAAT TATCTAAAAT TGAATATCTT CAGAAACATT AATGTTTATA
22651 TCATTATGTA TATGGACATT AAGAACATAA TAAAAATAAA TTTAGATGAT
22701 GAAGGCTTTC ATAATCTCAA TGTAAAATGC AAGAATAAAA AATATAAAAT
22751 TTATCAATGT ATAAAAATAA TGACAATATT TATATTATAT TTAATATCCT
22801 GCAATACAGT ACAATCAACT GTAATGTATA AAATAGAAGA AAGTTTAAAT
22851 ATGGAATAAT TAAAAGGAGG CAAATATGAG TCAGGTAAAG AATAAATAAG
22901 TATGATCAAT TATATTTAAG ATACACTGAC CTGAGTTTTA TGGAAAAATA
22951 TTAATGGTAA ACACCTTGTG GAGTGATTTC ACCATAATTT TATTAACTG
23001 TAAAAATATA TTAACATTTT CCCACAGGGA GTACAATTAA AGATTGTGG
23051 ATATTAGTCC TCCATGGGCT CAGCGTGGGA AAGTTAGAGG CTACAGCCTT
23101 TTCTGAATTA AAAGAGAAAC ATATAACTTT TTATTTATTT TTCTACAATT
23151 TAAAATTTGC AAAGGCATAT GAATGATTAC ATCCTAATAT TTGTCTGATT
23201 ATATAGAAAT GCATGACTGT CACCAGACAT CTGAAAGACA TCAAATGTCT
23251 AACAAGAAAC ATAAATTTTG TTTATAATCT TAGCCCTCTG TGAAATGCAG
23301 GGTTCACCAT TTTGAGTATA TTGTTCAAGC TACTTTCCCTA TAGCAGGTTT
23351 TTGCTCTCAT TCCAAGACCT GCAATTTCTG CTGAATGGGG TCAGGGTGCA
23401 CCCAGCTCAA GCCTCATCTG ACCCACTGAC AGGCTCAGTT ATCTCTGCC
23451 CAGGCAAGGG ATGGGCTTCT CTATCCAGGG CTGGATCCCC AGGGCCAGGC
23501 AATGTGGCTG AAACAAGCCA GTTCTTAGCA GGAAGACAT AACCTACCTG
23551 GGTGGCTATA AAATAGAAGG TCTGCACCTG AGCACATAGA GGCCGCCAGA
23601 ACCGGGCAAG CTGAGTGAGC TGCTCCCAGG TCAGTGGAGA ATGGACCTGC
23651 TGCACCGATA CCCAGTATAG GTCTTGATAA ATGGCCTTGA CACAGCTTGT
23701 AAAGTCACCA AGCTTTTCTG AAATGACAGC CATTGAATCT CTAGGGTCTG
23751 AGACCTGTGC TGCTTGGTGC ACCCAGTGTG AGTCATGAAA GGCCCTCTGT
23801 GGTGGGCATC ACAGGTCTCC TTGAGTTTAT TGCTGTGCAA AGTGGAGGAC
23851 TTTAGTTTCT TTTTCAACAT CAAGCTGTGC TCCTCTCCTG GACAGATCCC
23901 CGCAAAAGAA GCATGTGAGT GAGATACTCG CCAGCACAGT TCCCACCGAC
23951 CCTCATTTCC AAAACCTCCC ATGCACCTTC AGGTGAACAT TTGAATCTTC
24001 CCCTCCATCC TGACCATATT AGTACTTAAA TGAAGTGAAG TTTAACACCT
24051 TCTGAGTCCC CAAATATTCT CTGAGTGCCA GGATCTCAA AATTTTTTCA
24101 GTCACCTTGC TGCTCAAACC CTCTATAAAA GTCAACTGCT TATTTTCCCT
24151 TTGGGGGAAA AAGGCAAAAT TCTACCAGCT CTGTCTTGGC AGCTGTCCCT
24201 GGAACCGATT TTCCTTTTCT TGGAGTTTCC CTCATGTGAG CTCGACTCTG
24251 GTTCTGTTGA TAAAATAAGA GTTTGAGTAA GTGTCTCAA CCAAACACCC
24301 TAGAAGCCTT AGTTCATCCT GGACACAAAG GAGCTGAAGT AGCTATCAA
24351 CCCAGCTCTC CTCTGTTCTC CAGAATCCAT GTCTATATGG CCCTGGCTGC
24401 CAAAGAGCTC CCAGTTTCTT TGCCAGGGGA GACTGTGTTG CAGCCCTTTC
24451 TCTTTTTACC TTGAAAGAGT CAAATTTTAC CTAATCTAGC AGTGCTGTTT
24501 CTAGCTTTGG GCTTAGTTTT CTCAGAAATC TTCTCTTCAT TTAGATTGGG
24551 CTCTGATCCT AGTGCAACAT GGAATTTAGG TGAATCACTT CTCTCAGACA
24601 CAGAGTCTCA TAGTCTATCT CTGACAAATA TTTGTGGATC AGTCCTTTAA
24651 GTGAAGCTCT TCTGCCAGTG TCATAAGTGA AGATGTTTCT CAAAGTCTCC
24701 CCAGGGCTCT AAGCCATCTT CCATCCCCAA TTTCAAATAA AAACCTTACC
24751 CAGAGACACA CAGCTCAGTA TCCCTGATTC CAACACTCCT TCCAGCCTCC
24801 ATAGGAACAG CCAAGGCAT TACCCTGTCT TTGCCTGTGC TTCTCACTGG
24851 AATGGGAGGA GGGGGTCTCG GCTTTTTGTT TGAATGTCT CTCTTATCT
24901 GAGCCCTTTT CTGTAAAGGA GATCTGTTGG AAAGAAGGCT GGTCAAGTGG
24951 GCATTGGATG GAGGAGCAGT GGAGAATTAG GGTATTCATT TCCCTTTCCC
25001 TTGTTTAAGC TCAAGTGAAG GGTGCTCTCT CTTACACATC CAGATTTCAG
25051 CTGTGTGTTA TTCTGCTGGA CCTGCCTTTT ACATGTCTCT GGCTGGACGT
25101 GGCATACTCC TATTGACTGA ACAGTTTCCT TTTTCTTGCC ACTCATTAGG
25151 GCCTCATAAG AAAAGTTTCT TGCTGTAGTT TTACTAGGGA CCTAGACACA

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25201 GTTAAAGAGG GACATTTTCT GGGTCTTGTC ATAGTGTAAG AAAACCCCTAA
25251 ACAAACAAAA AACAAAGCCA GGGGCACAGG AATCAGAAAA TAGGGGAATC
25301 ATTTTCTTAA TTTCTGTCCC AATTCCACCT GGAAGTATTT ATGATACTGT
25351 TTATTTTTC AATATGCAGAA TTAAACATAC CTATATTGAA ATGTGTCATA
25401 CATTTGGCAA AGGAAGAGAA TTACACATAG TGTTAAAAATC ATGTACATAG
25451 ATATTATAAT TTTTCAAATG CTTGGAAATG TCAAATTAAG ATTATGGTTG
25501 ATTGTATTAA ATAGATACAT ATATGATAAC ATAAAAATAT GAAGAAAAAG
25551 TAAATACCAA ATAAAAATGGC TCAAATAATT AGAGATTAGA CAATTAATTA
25601 GACAATAATT AGATCAAATA CAATCAACTC GAATTTATTT AATTAGAGCA
25651 GATGCTAACT TAATCAGCGC CTGATTCCCTG AGGTAGCAAA AAGTCTAGGT
25701 GGAGAGAGAA ACTTACCCCT TTTCTTACCC TTCCTCGGTG ATCCTGGGAG
25751 CTCCACTTTC CTCTGTAGAA TTTATTTCAGC CTCCTTAGTA AACATGGACT
25801 TGGTCCCAAA CAGGTAACCC AACTGACCAC AAGAAAAGCA GCCTAGATCC
25851 TGAGCATTCA GCTCCTGTCT TCACACAACA GACACCACCT CAGTCCCATC
25901 AAAGCCTGTG AAGTTTCCCT ACATCCACCA TTGAGACATA TTCCAGAGCA
25951 GCCTCTCAAA ATTGCCTTAA CAGGATGGGA CACGATATGG TGGAGCTCCT
26001 GGCTCAGGAC AGCTGCCTCA CCCCTTCCTA CTGAGAAGTC TGTATCTGCT
26051 GGTAGAGACT ATCAAACCTGT AGAAGGCTTA GTGCCTGTCC CAGCAAGTGT
26101 CCCCTCAAAA GCCTTCTTGT TTTCTTTCCT TCTGAGAAAA GCATACAAGA
26151 ATGAGACCTT CTATGTTAGA GAGAACTCAG CCTCCACTCT CAATTGACTT
26201 GGTTGACTGA TGAATTGATG CCTGAGGAG GGGATAGATT CAGGGAAGAG
26251 ACTGTGCTGA ATGAGTCTGT GTTTTCCTAG CTTTGCTGTC TGTGCAAATA
26301 GTGGAACCCA GAAAAATATC GGGTGGTAGA CACACAGACA CTCTAATTGT
26351 CTGAATTTAA ATATTATTTA AATGGAACCT ATAGTATCAT TATATATTGA
26401 TACCATAATA TCACATAAAA TTTGTTTGAT ATATAAACAA ATATTGATAT
26451 TTTATCATAA TATCATAAAG CAGTTGTGCA CACAATAGCA GATAATATTC
26501 TCCGTTCTTA TAAAGTTTAT ATGTTAATGT TCTTACAAAA TTTAACTCAG
26551 TTATTTTATA AAATTACCTA ACAAATTTT GTTACTGTGC TATCATAATA
26601 ATACATAAAA CTATGAAATC ATAATATATT GTAATATAAT ACATATGAAT
26651 TATGATGTCA TAATGTATTA TATCACAATA CATATGAATT ATGCCATAAT
26701 ATATTATGTC ACAATACATA CAAATTATGT CATAATATAG TGTGACATCA
26751 TGATGCATGT GAATTATGAT GTCATAACAT ACTGTGATGC CACAATACAT
26801 ACAAATTATA TCATAATATA ATGTGATGTC ATAATATATT CATTATATT
26851 ATTTATGATT TTATAATAAC ATGAAATCTT GTCAGTTAAT TTTATAAGAA
26901 AATTGAGTTA AATTTTGTA CAACATTAAC ATATGTAGAA GCTTACAATC
26951 ATGGTGAAAG ATGAAAGATG AGCAGGCATC TCACATGGTA GGAGTGGGAA
27001 CAGGAAAGTT GGGATAAGGA TACGCCTCAT TTTTAAACCA CCGGATCTCA
27051 TGAATACTCA CCATGACAAG AACAGCACAG AGCCATGAGG AATCCATCCC
27101 CATGATTCAA ACACCTCCCA CCAGGCCCA CTTGTAACAT TAGGGATTAA
27151 AATACAATAT GAGATTGGGA ACAAATATCT AAATATATC GTATGACCAT
27201 TGGAAAAACA GATGAAACAT TCATGGTTTC TACTGTCCAG ATACTTTCAT
27251 TCCAGAGCAA ATGGCTAAAT GATTGCATT CACATTCTGA GGTCAGAAGA
27301 GAGAAGGGAG GTGTACAGGG GACTTTGGCT GCATTTGTTT CACTTCCCAT
27351 ATGCTGTTGT TGTGAGTTCT AACATTATCA CCAGAAAGGC TATTATGGGA
27401 CAGAAGAATT ATTGCTATTG TTGTGATTAT TTCTATTTCT TTTACATTAG
27451 TAAAAATAAT TTTTCTAGCT TCTCATATAA TTTTCTTAAA AAAGCCCTAA
27501 GAGTTTTTCG TAAATTCTCT GTTATTGTGT GTCATAAAAA TTGACAGGGA
27551 AATGGCTAAA ATAGATTAAA ATTACACAAA CTCTAGGAGT CAATTCTATC
27601 AGGCAGGCTT AGGAAAGACA GAACTGGAAA TACTCCACCA GCAGAACACG
27651 AGATGCATAG GGCCCACTTT CTGTCCCTGC TGTCCCCAGG TCCACCCTCT
27701 TCTAAGGCCT CCTCCAGGTC TGGCTTCACC CTAGAATCTC CTCTCACAGA
27751 ACTAATTAAA GGAGATCAGA AATTTGAGTG GTGACTCCTG CTGCCTCTCC
27801 TGGCTGTTGT CCCCCAATT CCTGCAATAA AAAAGCAGAT AAATGGGAGC
27851 AAATAGTTAT CTATTTGTGG GCCACAATT CTTTTTCATT GAAGCCATAG
27901 AGACATCCCA TCTAGCAACC TGTTTTTTAT TTTTGCATAT CCAGTAGTTG
27951 CTCTACAAGG CACAAGAAAG TCAATATAAA TACCAAAAAA TCCCTCTGGA
28001 ACAGTTCATC CTTTCTTTCT GTATCCCTTT CATCTGTCTA TACAGCTTTT
28051 ATTCCATACA TTTTCTTTT TAAAGTGAAT AAATTTAAAA AGTGAAAGAA
28101 AAAATAGAAA TGCTGGGCC TTTCTTCTAA TCCTAGAAAT TATGGAACAC
28151 AGCACCCTCT TTCCAGGGTG TGATGAGGAT TCACTCACAT CATGTAAAGT
28201 TTCCAGCACA GTGGTCTGTA ACAGACTTCT GAACACATAG TACATGCTTA
28251 ATAAGCATTG TATTAACCTCA TGTGTACATG TTTTCTTTT TTAATCCAGA
28301 CTACTCAAAA TGTTGATGCC TTCTCTAGCC TCTGTAATCT TTAAGAAGT

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28351 GGCAAAAAAT GACATGTTTG TAAATGGTGA TTGGTGGTGT CCACGTTGAG
28401 CCAAACTCT CTGTGCTGTG GTAAGAGTGT TGGGTATCAG GAATTCTGTG
28451 TGCTGTGCCT ACTTTCTCTA GATGATTGCT ACTACCACGG ATGTAGTGGG
28501 AGAAACATCA GCATTAAGAG GAGAATTTT AAGAGAAGCT ATTTACGGA
28551 CCCCTTTCCA AAAGTGC AAAATCACATCA CTAAGAAAAA GGCCTGGAAT
28601 CAGAAATGAT TTATATGTGC ATTGAAAAAT GAGGGGCAAT ACTTCTCTAG
28651 GTGGCTCTCA GAATAGGCTT TCAACTATAA TCACATGACC CCTTTAAAGA
28701 CCTACCCATA ACCTGTACCC TCCACCACAA GATCCTGTCT GTTGATCTTG
28751 GGTGGGAGCA TCCATATGGT TTTAATTAGG AAGTCAAATT GTCCCTCTTT
28801 GATGATTACA TAATATTATA TCTAGAAAAA TCTAAAGACC ACCAAAAACC
28851 TTTTAGATTG GATAAATGAA ATTTAATAAT GTTTCAGGAT TATTAATAAT
28901 CAATGTAGAA AAATTAGTAG CATTTTATA CACTAATAAT GATCAAGCTG
28951 AGAACCAAAT TAAAAAGTCA ATTCTTTTA CAATAGCTAC AAAAGTACCT
29001 GGAAATACAA TTAATCAAAC AGGTGAAAGA TATCTACAAG GAAAACTACA
29051 AAACATTGAT GAAAAAATT GTACATAATA CAAACAAATG AGAAAAACAT
29101 CCCTGCTAAT GGATTGGAAG AATTATCAT TAAAATGACCA TATTGCCCTC
29151 CAAAAATCTA CATATTAAAT GCAATTCCTA CCAAAATGCC AATGTTATTT
29201 TTCATAGAAT TAGCAAAAAGA ATTAAATTTA TTTGTAACCA TAGCAAAAGTC
29251 TGAATAGCCA AAGCACATTT AAGCAAAGAG AACAAAGTTG GAGATATTAC
29301 ACTACCTGAC TTAATAATTAT ACTAGAAAGC TTGAATAACC AACACAACAT
29351 GGTACTGATA CAAATAGACA CCCAGATCAA TGTAAGAGAA TAGAGAACCT
29401 AGAAATAAAG CCACGTACTG ATCATTTACA AAATCAATAA AAGCATACAT
29451 GGAAAAATGA CATCTATTTC AACATGTTGT GCTTGAAAAA TTATATTACC
29501 ACATGCAGAA GTATGAAATG GAACCCGTGA CTCTCACCAT GTAAAAAAT
29551 CAACTCAACA TGGATTAAAA GACTAAAATG TTAGACCTGA AATGATAAAA
29601 ATTCTAGAAG AAACCCAATG ATAAATGCTT CTGGACATTG GCCTGGGCAA
29651 ATAATTCATG ACCAAGATCT CAAAAGCAGA TGTAGCAATA ACAAATAAG
29701 ACAAATGGAA CTTAATTAAA CTAAAAAGTT CCTGAAAAGG AGCTTTTAAT
29751 TAGCAGGTGA GCAGACAACC CATGAAATGA GAAAAATGTT TGTGAACAT
29801 ACATGTGACA AAGAACTAAT GTCTACAATA TACAAGGAAA TCAAACAACA
29851 AGAATAAAAC AAGTAACCTC ACTATAAAGC AGGCAAAGAA TGAGAACAGA
29901 TATTTTTCAT ATAGAAGACA ATGATTGCCA AGAAGCATGT AAAAAATGTT
29951 AAACATTGCC AATGATCAGA GAAATTCCTA TTAATAATCG CAATGAAGTA
30001 CCATTTTATA CCATTATATA TGGCTAATTA TTAATAAGCA GAAAAATGAC
30051 AGATACTGGC AAGGATACAG AGAAAAGAGA ACATTATTC ATTGTTTCGAG
30101 GGAGTGTAAT TTTCTACAAC CTCTATGGCA AACAGTATAA AGATTTTTCAT
30151 GAAAACTAA AAATGGAATT TCCATTTGAT CCTGCACTTC CTCTACTGGG
30201 TATCTACCCG AAGGAAAATA ATTCATTACA TAAAGAAGAT ACCCACACTC
30251 ATATGTTTAT TGCAGCACTA TTCACAATAG CAACGATATG GAGTCAGTTT
30301 AAATTTATCA GTCAATGATT GGATAAAGAA AATGTACTAT ACATTTATTC
30351 CATGGAAAAC TACTCAGCCA TAAAGAATAA AATCATGTCT TTTGCAGCAA
30401 CATGAATGCA ACTGGAGGCC ATTATTGTAA GTGAAATAAT TCAGAAACAG
30451 AACATAAAGC ACTACATTTT CTTACTTACA AGTGGGAGCT CAATAATGCA
30501 TACACTTGGA CATAGAGATT GGAAAAATAG ACACTGGAGA CTCACAAATA
30551 TGGGAGGTTG GTAGAGGGGT TAGGAATGAG AAAATACCTA ACTGGGAAAA
30601 TGAGCACCGT TCAGATGATT GTTGACACAGA AGCCACACT TCATCCCTAT
30651 GCAACATGTC CCTGTAATGA AGCTACATTT ATACCCTCTA GTGTATTAAT
30701 AAAGAGAAAA AAAGTACTT TTTTTCAGTT TTGACAAGAG GGCAACTGAC
30751 AAGAGGGCAG ACTGAATAGA CTTTATAATT TTCATAAATA TTTATATTAG
30801 AAAATAAAT TTAATAAAAA TAAAAAATAA TATTGTATTT TTAAGAATGG
30851 TATAAAAAGA TAATTTGATG AATTGGAATA GTTAGGACTT AGCACATACA
30901 ATATGTTAAG CAAGATTCTA AGCCATTAGA CATTTGTAGA CAGAATATCT
30951 AACAGTATAA AATAAATAAC ACAAATATTC ATTGGCAATG ACAAATTGAC
31001 ATATTTTCAA TCCTATTAGA TGATATTAAA ACCATTACAA AATTTACTGT
31051 TTTGTTTCAT AATAAAAAATC GTAATGTAA ATAATTTTAT TTAATAAGTTT
31101 GACTAATTAG GCATATAGAG AAATGGGCAG TATGTTGACC AGTAAACAGG
31151 ATACAAATTA TTTTTCGAAA AGCAAACAAC ATTTTATATAT TTTATTTATTT
31201 TATTTATTTT TCTGGTCGGA GGAGCTGCTT TATTGTCTGA GGACATAGTA
31251 CGGTCTCTC CCTGGGAGGT GGGTCTTCC ACCGGTCACC CGAGGCAGTG
31301 TTCCAGGAGG CTCATGCAA CTTACTGCTG GGCTCAGCTG GGGGCTGGGC
31351 CTTGGAGAAG GCGAACTGTG CAGGGAAGCA GTAGCTGTGG GTCCTCACCG
31401 CCCGCTCTGC TTTGCTGCAC TGGGTCCCTG GTGCTCCTCG AAGTCCCACT
31451 GAGCCTGCGT CTCTATAGGA CGGTGACCAT CCAGCCCAGA ATCTTCTAGT

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31501 CAGAGCACAG TTTGACCAGG CCAGGCATTT CCGCTTCCTC TCCTTGGGCT
31551 GGACTTTGCA CTTGGGTTTC TTCCAGTCCT TCTTCTGCCG CCTGTCTGCC
31601 AGAGCTTAAA TTCCAGCCTC ACAAATGTTC CAGCTAGAAA AGGCGTGTCC
31651 GCGGCGCCTC GCACACTGGT CTCTTGGAAG GCACGGGCGG GTGGATTCTT
31701 CCAGGGCCAC CTGCAGGTCC GGGTGTGGG CCCTGTGAGC TCGACCCAC
31751 CCCTGCCCCC CGAGCCCATC CACTGAGCCA ACGGTATCCT CAGCCTTCAC
31801 TTGCTTCCAC CATCACACCG CCCTACAAAG CGGGTGTGCG CTCCTCAGCT
31851 CTCCTGCGAT GCCAGGAGCC GCCTCCTCCC CTACCCTGGC CCTGGGGTCC
31901 ATGCCACAG AACGCTGGGC AGAGGTGAAG GAACTGGGAA ATACCCCTTT
31951 CTCAAATGAC TTTGGGGTCC GCCTGGTCTT CTCTACTCCC TCCCACCCTA
32001 CCTGCACTGT TCCTTGGGGC CTGCAGTTTT AGCAAAGTTC CCTGCCCCCC
32051 ACCCGTGTCA GGAAGCAGTC CTGATGCCCC CTCCCACCCT TTCCCTCTT
32101 CTGGCCCATC CTCTCTCCCC ACTGGGTGAC TGACAGGAAT CCCTCTCCTC
32151 CCTGCTGTCC CTGGAGCCTG TCTGCTTTCC GCGCTCAGCC TCCTCCCTGA
32201 CCGCTTCTCC CTCCTTATCC TGAATCTCCC GACTCCCGTG GGGTGGCCCC
32251 CCCACCCATC CCGGGGCCCC GGCAAAACCG ACAAATTAT TTCAAATGGG
32301 AAGATCTGAA TTCCACTGAA GTCATGACAA CAGAAACCTT TGTGGTCATA
32351 TTTTAAAGAA TGATAGTAGC AACTATCCAT GTAAAGTATA ACTAGCCTTA
32401 AAAATACCCA CCACTTTGCC AAAACAACA ACAAACCAT GTTATAGCTG
32451 AAAACAAT TCAATAAACT TACAGGATAC AATATTAACA TGAAATCAG
32501 TTGCATTTTT GTACAGTAAC AACAAAGTAT CTGAGAAAGG AATAAAGAAA
32551 ACAATTCAT TTACAATATT ATCAAATAGA ATTAAATACT TAAGTCATTA
32601 AATAGAATGA GTTTAACGAA GAATAGTAAA GATCTGCATA CTGAAACTA
32651 TAAATGATG ATAAAAAATT GAAGAATACA AAATGAAAA TATATCCTGT
32701 GTTCATCGAT TCTAAAAATT AACATTGTTA AAATATCTAT ACTACATAAA
32751 GTTATGCTAC AGTTAAATAA ATTTCTATCA AAATTTTAAT GCCATTAAAA
32801 TAAATGTAAA ACAAAACATTT GTAAAATTAG TATGGAGCCA CAAAAGACCC
32851 CAAATAGCCA AATATTGAGA AGAATAAAAA GGCTGAAAGC CTCAAACCTC
32901 TTGATTTCAA ACAATATTAC AAAGCTATAC TCATCAAGAA AGTATAGTAC
32951 CTACATAGAA ACAAAATGGAA TAGAATAGAG GACCCAGAAA TAAATTCACA
33001 CATATACAGT AAACCTGATCC CACCAAATTA GGAAAAGATA GACACATCAA
33051 GAAATGGTGT TAGAAAAAAC TAGCTATGCA CACACAAAA AGTAAAGCCT
33101 TCTCTTATCA CAAAAATGAG TTTAAAAATA AGACATAAAC ATTATACTG
33151 AAATAATGAA TCCTCTAAAA AAAAAACAG GGAGAAAGCT CCTTGACACT
33201 GGGGGGGGCA NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
33251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
33301 NNNNNNNNNN CTAATAATAA CCTGTACTTG AAATTTGTTT ACAAAGTAG
33351 ATCTCAGGTG CCCTCACCAC ATACACAGAA ACGTATAAGG TAACATGTG
33401 TGGGGATAGA TATGTTAACC AGCTTGAGGT AATTTAAAGA TATATACACA
33451 TCTAAAAGCA CTCTATTGTA CACCTAAAC ATACATACTT TTCAATATGT
33501 AAATCATAGC TCAATAAATG TGGCGAAAAA ATTAAGAGTA ATCAGTAGGT
33551 CATATTTAGC CACAGGTACA CTTTATTTAA AACTCTCTTG TGAAGTGT
33601 CTGGCTGAAC CTGGGAACGC CCCCAGTACT TCTGACCCCT TGACTTCTCC
33651 AACACTACTT CTATTCTTCC TGTAGCTGGG GAAGATGTGA TAGTTCCCAA
33701 GAGTTTTATG GTTTCCAGGC CATGCAGATC TGGGAGGGCC ATCAGCCGTC
33751 CCCTTGCTCA TTGCGCACAG CTCCAGGCAA CCCATGTGAG GGCATCGCAT
33801 CCCGGCGAGG GCCACAGCAG ATAGCAGGGG CGAGGTAGCT CTGGCTGCC
33851 TGCAATCCAA TGGCCTCTGG CTCCACAGGC GTCCTTCAAG GCCCTACCAC
33901 AGCCCTCCT CTCATGACCA GTGAAGGCAA TGTAAGTGCA GAAGACACTG
33951 AGGAGGCAAG TAAGAAAAAA TCTTGGCCCC CGTGTATTAA TTATCATTAG
34001 ATCACCCCTG TTGTATACAG GATCACTCTT TATCATTACT GCTGTAAAC
34051 CTGCTACAA TGAAGAGAA AATGATCTGG AGCATACTCT TTGAATTCCT
34101 GAAGTTGCTG TCAGTAAGTT TCAGCAAAAA TTTATTCTGA CCATGATTTA
34151 CAAAGTTATG TCCTTGATA TCAAGGCAGT CAAAATGAAA CAATTGTAA
34201 TGGAAAACGG ATTGTTCCGGC TGACAACTAA ATGTGAGCCT TATGTACCTA
34251 AGCATAGACA TGAAATGAAA ATTGGAGAGA CTAGGTACC CTTTCACATT
34301 CACCTGGCA GTGATACTTG TGATGGCTGT GAACCACAGC AGGTTGGAAC
34351 TCACTTTCAC CTTGATAAGA GAGAGAATTG TTTATTGAAT TAATTGTTTA
34401 CAGCTAAGTA GGGGAAAAAA GAGTTGGAAA TAAGAAAATA ATTTTAAAA
34451 TGTGAGTAAA GTATGTTTTA CATTATACAG ACTATGAAGA TGAATAGACA
34501 TTGAAGAACC TGAAACATAA AGATACAGCT GGAAAAAGTA AGGAGCCTAT
34551 TGGAAGTGAA GAACACTTCC AAAGAGTTGA TGCACCTGCA TCTGTTTATT
34601 CTGAAATTAC TGACAGCAAC AAAAGTCAGA AGATGTTTGA GGAGGTGGGT

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34651 TGGAAAAAAG AAGAGGGCCT GGGGAAGGAT GGTGGAGGAA TGAAAACTCC
34701 AATTTTGCTT TAGCTTTAGC AGACACACGT AGGCTTGAGG ACAGGCAATT
34751 CCTCCTCAAT TGAAGATGTT CACCTTCTCC AAAACAAAAA CAAACTGGGA
34801 CAAAGCATGA GATAGGTTTT CTGAAAATTT CCCAGAAACT AAACCTTGAA
34851 AAGATGACCT AGGGACTAGG CCTTGGGTAA AAAGGGGCTG TCGAGTGAGG
34901 GTTAGTCATA GAAGAAAACT CAAGTTTTTT AAAAAATAGA GTTTGGAAAC
34951 TCTTATTTAT TTTATTTTAT TTTTTCGAGA ACTTTTCTCC CAAAAAGAGT
35001 CTGTGGCACA GTTTACCCCT TCCTGATTCA GAAATGTGTA ATAAAGTTTG
35051 GTTTGCAACT TTTCAATGCC ATTTTTTTAA ACTAATAAAT AGTGATTTAA
35101 TCAAGTTATG CAGTAAGTGG ACTAAAGTTT ACAGGGCACA CATGAAGTGT
35151 GTCACACTTC ATTATTTTAT CGTGTCTGCT ATGACATCCC TGTGAGCACA
35201 AAGCCCTCTA TGCACAATTC ATATTACCAC TACTGACGTC AATATACATC
35251 TTGTCTCTGT CTCCTCCTTT CCCAGCANGA CCCCAGCAG NAGAAATATT
35301 CAAAGTGTTA AAATAAATCT GCTGTATGCA TCCTNNNNNN NNNNNNNNN
35351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
35401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNCCATTT ACAATATTAT
35451 CAAATAGAAT TAAATACTTA AGTCATTAAA TAGAATGAGT TTAACGAAGA
35501 ATAGTAAAGA TCTGCATACT GAAAACTATA AAATGATGAT AAAAAATTGA
35551 AGAATACAAA ATGGAAAATA TATCCTGTGT TCATCGATTC TAAAAATTAA
35601 CATTTGTTAA ATATCTATAC TACATAAAGT TATCTACAGT TAAATAAATT
35651 TCTATCAAAA TTTTAATGCC ATTAATAATA ATGTAAACA AACATTTGTA
35701 AAATTAGTAT GGAGCCACAA AAGACCCCAA ATAGCCAAAT ATTGAGAAGA
35751 ATAAAAAGGC TGAAAGCCTC AAACCTTCTG ATTTCAAACA ATATTACAAA
35801 GCTATACTCA TCAAGAAAGT ATAGTACCTA CATAGAAACA AATGGAATAG
35851 AATAGAGGAC CCAGAAATAA ATTCACACAT ATACAGTAAA CTGATCCCAC
35901 CAAATTAGGA AAAGATAGAC ACATCAAGAA ATGGTGTTAG AAAAACTAG
35951 CTATGCACAC ACAAAAAAGT AAAGCCTTCT CTATCACAA AAATGAGTTT
36001 AAAATAAAGA CATAAACATT AGAACTGAAA TAATGAATCC TCTAAAAAAA
36051 AAAACAGGGA GAAAGCTCCC TTGACACTGG TGGTGGCAAC GATGTTTTGG
36101 CTTTGACAGA AAGAACACAA GCAACTAATG CAAAAATAAA AAAGTGGAGC
36151 TATATCAAAG TAAAAACTTT CTCCACAATA AAGAAAACAA TCAACAAAAT
36201 ATAAAGACAA TATATGGGAT GGAAGAAAAT ATTTGTAAAC CATATGTAGG
36251 ATAAGATGTT GCTATCCAAA ATATACATAA CACTAGTCAA TGTGGAAAAA
36301 AAAACTCACA CGAGAACAAA ACAAAAACCA ATTTCTGAT AAACCTGGCA
36351 AAATATCTGA ATAGATGTTT TCCCAAAGAC ATACAAGTGG CCAGCAGGTA
36401 TATAAAAAGA TTCTCAACAT TGCTAATTAT CAAAGTAATG AAAATCAAAA
36451 TCACAATGAG ATATCACCTC ATCGTGGTGT TAGCACAGCT ATTATCAAAA
36501 ATTCAAAATA CAAAAAGTGT TAGGGTGCAG AGAAAGGAGA ATATTTGTCC
36551 ACCATTGCTG AACATGCTCA CTGGTGCAGC CATTATAAAC AAAAAACAA
36601 CACAAAAAAA CAAACAAGAA AACCAGTAGG GAGGTTCTTT AAAATTTTAA
36651 AACTAGAAGT ATCTTTAATC CCAATTTGGA GTATACAGCC AATAGACATA
36701 AAATTAGTAT CACCAAGCGT ACCTGCACTC CTCTGATACA AATAAATAGG
36751 TAACTGTGA GAAAGAGATA ATTTAGCTT TAATAAAGAA TGAAATTGTT
36801 TCATTTACAA CAATGTTGAT GAACCTTGAA GACATTATGC TAAGTGAAAT
36851 AAGCGAAATA CAGAAAGACA AATACTGCTT GATCTCATTT TAATGTGAAA
36901 TCTTAAAGAA AGAAAGAAAA AGAAAGAAAG AAAGAAAAAA TGAAACAGAG
36951 ACTAGAATGG TAGTTACCAT GGGCTAAGAA TTGGGGAAAA GTGGGGAGAT
37001 ACCCATCGAA GGGTGCATAC CTTCAGTTAC ATAATAAAAA ACTTCTGGGG
37051 ACCTTATGTG CAGAATGGTG ACTATAGCTA ATAATAACCT GTACTTGAAA
37101 TTTGTTTACA AAAGTAGATC TCAGGTGCCC TCACCACATA CACAGAAACG
37151 TATAAGGTAA CTATGTGTGG GGATAGATAT GTTAACCAGC TTGAGGTAAT
37201 TTAAAGATAT ATACACATCT AAAAGCACTC TATTGTACAC CCTAAACATA
37251 CATACTTTTC AATATGTAAA TCATAGCTCA ATAAATGTGG CGAAAAAATT
37301 AAGAGTAATC AGTAGGTCAT ATTTAGCCAC AGGTACACTT TATTTAAAC
37351 TCTCTTGTGA ACTGTTTCTG GCTGAACCTG GGAACGCCCC CAGTACTTCT
37401 GACCCCTTGA CTTCTCCAAC ACTACTTCTA TTCTTCTGT AGCTGGGGAA
37451 GATGTGATAG TTCNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
37501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
37551 NNNNNNNNNN NNNAAGGATG GTGGAGGAAT GAAAACTCCA ATTTTGCTTT
37601 AGCTTTAGCA GACACAGTA GGCTTGAGGA CAGGCAATTC CTCCTCAATT
37651 GAAGATGTTT ACCTTCTCCA AAACAAAAAC AAACCTGGGAC AAAGCATGAG
37701 ATAGGTTTTT TGAAATTTT CCAGAAACTA AACCTTGAAA AGATGACCTA
37751 GGGACTAGGC CTTGGGTAAA AAGGGGCTGT CGAGTGAGGG TTAGTCATAG

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37801 AAGAAACTC AAGTTTTTTA AAAAATAGAG TTTGGAACT CTTATTTATT
37851 TTATTTTATT TTTTGCAGAA CTTTTCTCCC AAAAGAGTC TGTGGCACAG
37901 TTTACCCCTT CCTGATTCAG AAATGTGTAA TAAAGTTTGG TTTGCAACTT
37951 TTCAATGCCA TTTTTTTAAA CTAATAAATA GTGATTGAAT CAAGTTATGC
38001 AGTAAGTGGG CTAAAGTTTA CAGGGCACAG ATGAGTTTGT CAAACTTCAT
38051 TATTTTATCG TGTCATTTAT GACATCCATG TAAGCAAAA GCCATATAAG
38101 CAAAATTCAT ATAACCACTA ATGACTTAAA TATACATTTG TCTTTGTCTC
38151 CATATATTTCA CAGTAAGACC CACAGCAAAA GAAATATCAA AAGTTTATAA
38201 AAATAAATCT GGCTATATGC ATTCTTGTTC ATGCCCTTTA GAACCTAGAT
38251 AAAAGGACCT TTATAATAAA GGTCTAAATA ATACCATTTA AAGCCTAAAT
38301 AATACTATTT AGGCTAAATA AATAAATAAA GGTCCAAATA ATACTATTTA
38351 AAGCCTAAAT AATACTATCG AAGAACTAAC GAACAGGTGA CATACTATAG
38401 AAAAGTAGTC TTTTACTGTT TTCTTCTGTA AAGAATCTGT TGTTTGTGTC
38451 TATATATTTCA GCATTTATAT TTCATTTGTT TCATAGCTAA TGAAATATTT
38501 AGATATGAAC AACTGAGTAC AGTACTGAAA TAGTGCACTG GCATTTGTAA
38551 TTTTATAAAA TATTATTGCA GGCAGTGGAG TTGTGCCAGA GAAATCTGAT
38601 TTCTAGTACA AAAGGAATAC TTAGCTAGGG CCTGAAGTTT AAGATATTTA
38651 TTGAACATGT CCTCAATTGC AATATAAACA TTATAACATT TTTTAAAAAT
38701 TCTTTTAAAT ACATTCTGAA TTAAACAAAA ATTTCAAATC ATACCTTTTA
38751 TGAAGTAGG GAAGTGCTAA TGAGGTAGAA TGGCAGTTGA AGCCAAAACA
38801 TCTGAATTTA TGTAAATAAT TTTACCCACA TTAGTTTTTT GTTAAAGGAA
38851 ACAATAATTC TCACCATATA CTATTTACTG CAGTGAAGTA TTTTCAGAAA
38901 CGTGTGCATA ATACATAATT AATTTTCTAA TGGTAATACA TTCTACAAAT
38951 TATTACAATT GTGGTTTCTT GAAGAGAGCA GTATTTCAA TGAAGAACT
39001 TGGAATTTCT CATGAGGGGA TGATCATGAG GATGATCATG AGGGGATGTC
39051 AAATCCATGT GGGTTGTTCA GTTCTAACA AGACAAATGG AATAACATA
39101 GATGAAGTGA CTGCAGGCAT CCCAGTGTG CTGTCTTCCA TATGTGAGAA
39151 CAAAATTATA AATTATGTTA CACAAAAGGA GATAAGTTAC TAGTGTGAAG
39201 CGTTAGATAA ATTATATGGC ACATAAACT GAGATATGAG GTTTGTATTT
39251 ACATGATTGA CAATATAATA AAAAAAGAAA CAAAATAAT GTGGAAAAGA
39301 ACTACGAGAT TGTAAATCA TATTTGGAAA AGAGGCAAAT GGAAAGTAAA
39351 CTATTGAAAA TGTAAGTAAA CTACTGTACA GCATACAAAT TACACATTAA
39401 AATAGGCTGA GCTGATGAGT AGGACTAATA AACTGAAACG CTGAGCACA
39451 TTAATGTAGT CATATAGTTT TTAGAAGGCA AATTAATACA AAATACAAAT
39501 ATATTTATTT ATATAGTGAAG ATTAGCTGGG AAGAAATGAA AAATAATTTG
39551 TTTTACTAGA CTATATAAAC AGGAAGGTAA TATTCAAAA ATCAGTGACT
39601 CATAAGTTTC AGAAATTGGA AACACATGAA TCCTATCAA GAAATAATGG
39651 TTTTGGTTAT TGTGAATACT GCTTCAATAA ACATGGGAGT GCAATTGTCT
39701 CTTTGACATA CTGATTTTAT TTCCTTTTGA TATATACCCA GTGGTGAGAT
39751 TGCTGGGTCG TATATATGGT AGTTCTATTT ATAATGTCTT GAAAAATTTT
39801 CATGCTGCTT TTCCTACCTG GCCGGGGCTC CGACAGCTGG GCATCCGGCC
39851 GCAGTCCCTC TCTCAGGATC CCTCCACCCT CCGCCTCCCA ACAGTTCGGG
39901 CTTTTGTGTA CGCTGTGGCT GCTGCTTCTG CTGCCGAAGC TTGGCATTGG
39951 AGACACCTCG TCCTCCTCTC AGGACAGATC CATGAACCCA TCGGCAGCGG
40001 CGGTGAGCGA TGCCTTCCCT CTGCCACAAG GCGCCGCCTG CAGAGCCTGC
40051 CGCGTCCGCC ACGCCAGAG CGTACCCGCA GCTCAGCGCC GAGTTACTCC
40101 TACTGGCGGT GGCCAGGGAG TGACTGGAGT CGCCGGACAC CCCTGGGGAG
40151 CAGGCGAAGG AGGAGCTGCA GCCACCACGT CCTCTCTTTC CCCAGGGATG
40201 TGCAGAATTA CCATGAAATT ATGACTCCTC ATCCTAAGAA TTACCAATGG
40251 GAAAATTGGA GTCTAGAAAA TGTTGCCATC ATTTTAGCCC ACCGGTTCCTC
40301 CAATAGCTGT ATTTAGGTGA TAAAGTGCTC TCGAATGCAT TGCACAGACT
40351 CAGTTGCCAT GACGATTTTG TGAAAAGTAA CATGTTTGGT TCCCCAGAAC
40401 ACAATACTGA CTCTGGAGCT TTTAAGCACC TTTGTATTAT TAGTTAATGC
40451 TTTTAAGTCA TAATAGTTTA TCAAAGAAAA ATTTGAACGG TTGGAATAAG
40501 GACTCCACGC ATGTAATTGC AGTCCAGTTT CCTGATATTA CAAATCGTTT
40551 CCAGGGAGAA AAAGAGAGGA CCTGTGAAAA ACCTGATGAG TTGGCTATGA
40601 GTTTTATATCC ACCATCACTA AATGATGCAT CTTTAAATTT GACTGGATTC
40651 AATAAAGATT GTGTTGTTTT GAATCAGTTT CTTTTTGAAT TGAAAGAAGC
40701 CAAGAAACGC AAAGACATAG ATACTTCCAT TAAAAGCATA AGAACAATAT
40751 ATTGGCTGGA GGGTGGTCAT TCCGTAGGAA GTAATACCTG GGTACTTAT
40801 CCACAAGTCT TGAAAGAATT TGTACAGTGA GAGATTATTG TTCACACCCA
40851 TGTAACACTT CACCAAGTAC ATGATCCAAA GAGATCTTGG ATTGGAAGG
40901 AGCAAAATAA ATTTGCTTAG ATACTTGGGG ATATTGGTAT GCAGGTGACT

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40951 AGCTGAATTC ATTTTCATGAA GGAAGCTCCC TGTATAGAGA ATCCCTTTAG
41001 AGTTCATGAA GTAGTTTGAG GCTACAAATA TATTGATGTA CTTGTTCAGT
41051 GGAAGAGCAT AAGCACTTTG AGTGTATGA ATTCAGATAA TGGAATGTAA
41101 TTCATAGGTG CATTGTCACT ATGGGGGAAA CACACGTTCC TGAATATGA
41151 GTGAAATATG CAATAGTATT TCTTCCTTGG GAATGTGAGC AGTTTTTAAT
41201 TTGTGTTGAG TTAGAATTAG TTAATTTAAA ATCTAACAAG GTGGTTTGAG
41251 ATAATACTGA GGAGATATAA GACCCTTAAA AGGAAAGTTA CAACATAGTA
41301 CTTCTAGAAT ATAACATAAA TTGTTTCTGT TGGAAATAGT GATTCTCTGA
41351 GTAATGTTAC TAATCGTGGT GATATTTTAA CAGTAATTAG CTATTTTGGC
41401 ACTTAAAACT TGAATGGAAA CAGTTTATTT CTCTTCAAAC AAAAGCAAAG
41451 GCACAATGTT GTTTCCTATC ATTTTGGAAT AACTGTACCC TGCCTCTTGT
41501 GTTTTGTAAG CTCATTCCTT CATTCTTTAA TGTGCCACCA AGTACTTTTT
41551 TCTTGAGAGT CAAAATATAT TTGTTTCACA ATGTCCAAA ATGTGCAAGA
41601 ATGTAAAGCT GTTTTTTAAA AACATAGCCA TGTGATGCA TGTGCCGTTA
41651 GTCCAGCTA CTCAGGAGGC TAAGGCAGAA GGATCCTTTG AGTCCAGGCT
41701 ATAACGCACC ATGATTGTGT TTGTGACTAG CTACTGCACT CCAGCCTAAG
41751 CAACATAGTG AGACCTCATC TCAAAAAAAA AAAAAAGAA AAAGAAAAGA
41801 AGAAAAAAA GAAAAACAGA ACAAATTAGA CTTAAGTACC ATCACTTAAT
41851 TTTTAGTTGA CAGTCTTTAG TTGATTGTTT TGGATAAGAC ATTCTGGGGC
41901 TTCTTGAATC TTGGCCAAA ACCAGTTGTT TTTGAAAAC GTTTTAAATT
41951 AAGCATATTT ATGTATTTTG GATAAAAATC AACTACAAAG AAAATTTTAT
42001 TTTTTCATT ATATTAGTCT TTTTGAAAGA GAACAACTTA GGGAAGATAA
42051 ATATATAATG CTCTATTTGT CAATGCTGTA TTA AAAAGGA AACAGATTTC
42101 ATAAATCTAA ATCAATGTTT CTCCACAATC ATGACTTTGT CTCAAAAAAA
42151 AAGTTATTTT TGGCCAAAAT GCAAAATTAT ATTGCTGTGA CAAAAGTCAC
42201 AAGGAATCGC TTAACATCA TCCAGCCTGA GGCCAGATCA ACATATGACA
42251 GTCACAATTT CAACTCTGAA CTGCATCCAT GTGTGAGATT TAGAGTCTCA
42301 TTAGTGGACT CTGCCCATGT ATGAGTTTGA CAATCCTAAT TGTTTTCTAC
42351 ATGTGTCTAT GAGTGTCA CAAGTCACTGT TTGCTGGGCC CTGTTATGTA
42401 ACTCTCTCTA AACCCCAAGG GGTTTATAAA ATACATGTGA GTGTCATAAT
42451 CTTCTGTGGC CATTTTAGAA TTAGTAGACC AAGGACCTTA GTTGTGCGCG
42501 TAAGCCTAGC TATTAAAGTC AAAATTACTC CTCCTGGCTG GGTCCATGTA
42551 AGAAAGCTAT CATCATGACT GTGGCCTGGG CCTAGGTATA CGTCACACCC
42601 CACCTGTGAG CAGAAACAGG GAGGAAAACC ACATCATCTG AATGCTGGGA
42651 CAGGGAATG TCAATATTGC TCAATTGGTA GGACCCACAC AGGAAAGTCA
42701 CATCACCTTT GTGCTAGGCT CAGTGATATG TCACAATGCC CACTGTAGAC
42751 AGAACCTTGT CAAAAGAGTC ATATCACCTA GGTGCTGAGC CCAGCAATAT
42801 GTCACAATCC CCCTTGTAA CAGGGCCAG TCATGAGAGG AGAGTCTTAT
42851 CACCTAGATG ATATGCCAG ATTTCTGTTA CAAACCTTAC TGGAGGCAGG
42901 GCACAGGCAG GAAAGTAGAG TATCATCACT CAGGTGATGG GCTCACAGGC
42951 ACATTACAAT GTCCCTTGTG GGTATGATCC AGACAGGACA GTCACATCAG
43001 CTCAGTGTTC GGGTCAGTTG TATGTAATAA TCCCAACTGT TGGCAGGGCT
43051 CATGCAAGGG AGTAAAGTCA ATCAAGTGGT GAGAAAAAAA TTGTATTTCA
43101 AAGTCACACC TACAGGAAAG TCCAGGGATG AGATTCACAG TCCACACAT
43151 TTTCTGACTC CTAGGATAAG AGACAACAGC TTCTTTGAAT TTGTGTTAAAG
43201 TACACAAATC ACAATCTCAA TGGTGGACAG AATTCATGCA TGAAAGCTCC
43251 AAACACACCT GCAAAACACTG TCTAATTAGA GCAGCCACGA TCTCACAGGT
43301 GTGCTGAATT TTGATATATA AGTCACCATT CTACCTGTGA ACTGTATCCA
43351 TGTATGAGAG TCACAATGTG AACTTTCAAC TGATCTGGGT ATGATATTCA
43401 GAACCTCAAC AATGGTCTAT GTCCCTATAG GAAGATGACA TTCCTCTCTG
43451 TATGTCGTGT GTGCTTGGAA GAGTCAAAAT GTCACCTGTG TGCTGGGCCT
43501 TTATTAGTCA CCTTCTGTGC CACTTAATGG CTTCATATGG TCTGCATGAG
43551 AATGAAAACC TGCTCTAAGA TTTCATGATG GCATAAACCC ATGATCCTAC
43601 ATGTTGCCCT AAGTTGAGGC ATGAGAGTCA AAACCTGTCT TATTTGCTGG
43651 CTCCATGTAT GAGAGTCATC AGTGTGCCTG TGAACGGGT TCAGAAATGA
43701 GCCACCATCC CATTTGTGGA TGGATCCAGA TATGACAGTC ACAATTCCAA
43751 CTGGGAAATG TTTCTGTAAG TGAGATCCAG GGCCTCGTGA GTGGGTTCTG
43801 TTCACATCTG TAATCTTTAT ACAATTAGGA GATGCAGAAC CTTACTGATT
43851 GTTCTATGAG AGTAAAAATA TCTTCTACTG GCTGGGCCCT CATATGAGAG
43901 TCTTCTATTAT TCCTGTGACC TGAACCTAGG GATATGTCAC AATCTTACCT
43951 GTGAGTAGAA CCAGGCAGGA GAGTCTCATC AGCTGAATAC TGAGCCAGGG
44001 ATATATTAGT GTTCCCCCTG TGGTTGAGTG CTGGTAGGAT ATTCACATCA
44051 CTATGGTGCT GGGACAAGTG ATGTGTCACA ATGTCCCTG TGGGCAGAAC

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44101 CCAGGCTAAG CATTACATCA CACGAGTGCT GGGCTCATCA ATATGTCACA
44151 ATACCCTTGG GAATGGGGCC CAGGCAGGAG AGTACAATAA CATCATCTGG
44201 AAATGGGATG AAAGGAATAT CACAAAGCCA CCTGTGAGAA GGGACTAGGC
44251 AGGAGGGCTG CATTACTGGG GTTATGGGTA TAGTATATGT CACGATCCAC
44301 ACTGTGGGTT ATAGAGAGAC AATATATTCA TCTCAGTTTA TTTGCGGGTG
44351 GACAAAAGTA TATGTCAGTC ACACATGTGG GAAGGTCTAG AAATAAAATT
44401 TACATTCCTA CAGATGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
44451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
44501 NNNNNNNNNN NNNNNNTAAT TTCTGGCTGG ACAAAGTATA TGTCAGTCAC
44551 ACATGTGGGA AGGTCTAGGA ATAAAAGTTA CATTCTGCA GTATGTTCTG
44601 GGTCAGGTA TAAAAGTATG CACCTCATAA ACTTTTACAC ACCTCATTTG
44651 CCCAAGTTTG CAAGTCATGA TATCAACAGT AAATTGGATC CATACATGAA
44701 AGACTCAACC TCAAACAACA CACATTAGAA GAGTTAGAGC CTAACATATT
44751 TGCTGAATCT TAGTCAGAGA CTCATCATCT CACCTGAAGG CTGGACCCAC
44801 ATATAAGAGT AATAATACCA CCTTTGGACT GCCTTTGGGT GTGAAATTCA
44851 GAAATTCAAT GGTGGGCTGT GTCCATGTGG GAGTGTGAAA AACTTTACTG
44901 TCAGGAGTGT ATGCAATGAG AGTCAAACCT TCAACACTGT ACTGGGCCCTT
44951 GTTTTATTAT TCTTGCACC ATCTGTGGGT TTTTATACTA CGTGTGAGAC
45001 TTGCAATCCA CTCTGAAGCA TTTGTCCTTG TATAAACCCA TGATCTTACT
45051 GTTAGCTAAG TGTGCAGACA AGAGTCACAA TTTTGTGTTGT GTTATGGACC
45101 CTGTTATGAA ACTCTCTTTA CCACCTGAGA GCAATGTGCA ATATGCTTGA
45151 GTGTTGTAGG GCTCTGTGAC TTTTGTACAA TTAAGAAACC CAGAACACTA
45201 CCTGTTGCC TAAGCCTAGT TACTAAAGCA AACATCTATT TTATTGGCTG
45251 GGTCCAGGTA TGAGAGTCAT TACTGGACCT GTGAGCTGGG TCCAGAAATG
45301 AGTCACCATA CCACCTGTGG CCAGATTTAC ATATAGCAGT CACAATTCCA
45351 ACTGTGGACT TCATCTGCAT GTGAGATTCA GGAGCTCACC ACTGGGCTCC
45401 CTTTCATGCAT GAGGGTGACA ATTCTAAATT TCAGCAGGAT GTGGCTACAA
45451 GAGTCACAAC ATCACCTGTG CTCTGGTTTG TATTATGAAA CTCTCTGTAC
45501 CACCCAAAGG CTTTATAATA TACGTGTGTG TGTCAGAATC TCCTGTAACG
45551 TTTTACAAGT AGGAGACTCA GGACCTTACC CTTTGCCCTA AATCTATCTA
45601 TAAGAGTCAA AATATCTTCT ATCAGATGGA TCCACATCTG AAAGGCATCA
45651 TGATTCCTGT GTGCTGGGCC TAGTAAAGGT CACAATCTTA GCTGTGGGTG
45701 AACAGAAGGC AAGAGAGTCA CATCACCTGG GTGACGGGCA AGAGATATAT
45751 TACAATCCCT TCTGTTGACA GGTCCCAAAC AAGGAGTTAC ATCACCTGGA
45801 TGCTTGGCTC TGTGATATGT CACATTGCCC AGTGCAGGCA GGGCACAGGC
45851 AGGAGAGTCA CATTACCTGG GTGCTTGGCC CAGTGCTATG TCACATTCCC
45901 TTACTTAGGG AGGGCACAGG TAGCTAAAGG GAGTCATATT ACCTAGGTAC
45951 TGGGCTAGAG CTATCAGTCT GTTGGTCATT CAGGGTGAGG GTTATGATCT
46001 CTTTAGACAT CCATGTAACA GAGCCCCAAC TCGTTCATCC TCAGAAGCAA
46051 AGGCCAGTGG AGACCAAATA AGGCTTGAAA GTTAAGTCCT CTAAAAAGGC
46101 AGAATGTCCT AGGCTTTGGC CTCTCCTCTT TAAGCACAA CAGATCATAA
46151 CCTCTCTTTT GACTTCTCAC TATGCCGCTC ACTGGAACAA GGCTCCTGAC
46201 TCCACACCCT CGTCTTTTCA CCCCTGTACA TTTATTGGGC AGACCAAAGA
46251 CCCGGAGACC TGAACCTCTG GACAGTCTGG GGAGAAGCGA ATCCAAAAAG
46301 GGTGCGGGCA GCAACGGCTG AGCTCCCACA GATGCCCCGG CCCAAACTG
46351 CAGGCCCAGG CTGTGGTCCA TGTGGCACTC AGTGCAGGTT CTGCAATGCC
46401 ACTGGAAGGC CTAGAAAATC CACTTCAGCT GCTGCTTCTT CCTTTTCTTA
46451 AGCGCTGAAA GGTATACACT TTCCCAAGCT TTTCAGATAC GGCCAGGCAC
46501 CCCCACCTGA AAAGGGGGAT AATCGCATT CTTATCATGG TTTATCACCT
46551 CACCCAAGCA CCAGCCAGCC CCAGCCTCGC CAATCCAGCT GCCCAGGCT
46601 GGAGGAGATC CTGTCAAGCC TCCTCTCTGA AACTCCACTC CTCTCTTTT
46651 TTTTCTTCTT CAACCACTGG CATACTTTTG GTCATCTTAC TTTTCATCCC
46701 AATGGGGCAC CTGATACCAT AAAGACCTGG GAACCCCACT GATCACAGGT
46751 CCTACAGGGG TCAGGCAAAC ATACAGGAAG TCCAGAAGGA CAGTCATCTG
46801 CCACCTCCAG TATGAGAAGA ACAAACCCCC CGCACTCCAT GAAGAAGTCA
46851 GGAACCCAGT GAAGGCTGCA GGTCCAGCCC ACAACAACCT ATGTATGTGG
46901 GGTGCTCCAT GGCTCATACG TGTGTCCTGC AGGCTGGAGC CCAAGCGAGG
46951 GTTCGCAATC TTTGTTCCAG ATGGGGAAC ACTACTTCAG CTTATTACCC
47001 AGGCTCCCTG ATGGGGAAAG GAAGGAAATG GCGAGAATCT TCAGCACAGC
47051 AAATCCCATC GTCCTGGCAG AGACAACCTC TGCCTGCATG CCACACCAGC
47101 AGCCGAGGC TAGAGGCACT CACATCAGGC CTCCCTCTTA CAACATTTTG
47151 TTTTGTGTTT TTTTTCGAAA GGCCCTAATC ACCTACTTTC GGTATCCTC
47201 CTTGTCACAA TAGGGCACCT GACGCCATAG AGACTCGAGA AATGTACAGA

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47251 TCTGGGGTCC TGAAGCGTCC AGGCGAAGGT GCTGGGAGTC AGGGAGGAAA
47301 GTCCTTTGAA GCCTCCAGAA GCAATGTAAC AAGACCCAGC ACTGCAGGAA
47351 GAAGTGGGGC ACCCAGTGGC AAATGCAGGC CTACGTGCAA GGTGCTCCCT
47401 GTCCCTCGCC TGCTCCCTGG AACCTGGAGC CGCACCTAGG ATGGGGGGTC
47451 TCCATTCCAG ACCCAGAATA AGCTCTTGGC TACCTCACCC AGCACCTGGT
47501 CATGCCAGAC AGAATCTTGG CTGGGGCTTT CTCATGGTCT GCAGTGCCTT
47551 CCACTTTGGG CCACCGTAAT AACACTTCTC CCACAGGAC TCTGCAGTGT
47601 CCAGCTCACC AGCCTGGAGT TTCTCATCAC CCAGTGATTC CAAAAGAAAC
47651 AATCTACAAT GGCATGAGCC CAAGTGCCAG AAACAAACAA ACAAATATC
47701 TGAGGTAAAGT CCATTGGTTA CTTGATTTT TCAAAGGTAA CATTGTCCC
47751 TCCTTGAAAT CCTAAGAGTG CATGAACAGG CTATTCTAAT GGACGTGAAA
47801 TTCACATTAA AACTGATTGA CAGATGAATT CTGATTCCAA GGTACTGTTG
47851 TATTCTCAA TTGCATCTGC TTACCCTGCC CCCCTCAAAA TGGAAGAGTG
47901 ATGACTATTT GTCATCTTAG CACTGTGGG ATGCAGAGCC TTAGATGGAA
47951 GTGTGTAAA AACAAACATTC CATAAAGGGC TGTCACCTCC AATTTTCAAG
48001 CAAGGTGGGA AACCAACCGT GATGTATGAA ACACCTGCTGG CCAATGTGCA
48051 CAATTAGTGA TACAAAATTG AATAATATAA ACTATTGTAA ATATGTGTGG
48101 ACATTGTGGC AATTTGGACA CCAAATAACA CTGCCAAAT CAGGAAGAGA
48151 AAGCTGTAAC CTCATGGTTG TTATGAAGCT TAACCTCTGG GTAGTAGAAC
48201 CTATCAAAAT TTCTCCATGC CAATCTGTCC AAACAAACAT TGAGATGTTT
48251 ATTTCTATAA AATTCTATA GAATCTTCTT GGGCATGACC CTTCTAGCCC
48301 CATCCTCACA GCACTGGTGC CAGAGGAAGT GCACTTGCTC CTGCCCTCCC
48351 CTATATTTTT AGGAGTGGAA ATATTTAGTG ACAGGATGGA TTGGGAGGGT
48401 ACTGAGGCCT CCTGGGTGGG TGGGTGAGT CTAAGTGCAGC CCAAGCCTTT
48451 TTATAATAAA TAACCTATAG GTAAATTAGA AAAGAATAAA AAATGCAACT
48501 CATTCCTCTT CTTTGCTCAC CACAAAGCAG TAAACACAGC ATCTAGAGAT
48551 GCTGTGGAG CCAGGCTTGT CCTGGGAAAG TAAGAAGTGC TTATCAGGAG
48601 CCCTGGGATT GAGGGCAGGT GAGATGGGTT CCCAGGAAGA TACAGCCAGG
48651 GTCAGGTCTG GCCCCTCAC ACTGGAAGGG GCCTTCTGAA GGCCAGGAAA
48701 AATGGTCCAG GTCAGTAAA CTCAAGCGGC CCATCTGAGC CAAAGATCTG
48751 TCCAGGTGCG AGTGAATCTC ATCAGCACTG CCAATAGGGG GTCTGATCAG
48801 CCCTGAAGAG CTCCATCAAT GGAGGCAGAT GGCTGGTGGG TGGGTGAGGA
48851 GAGCTGCCTA CTGCCAATGT GGGAGTCCAC TCGGTGTGGG TTTACTGCGC
48901 CTCTCAGTGG CTGGATAAC CTGCTGAGGC TGCAGCTTCT TCCCCTTTT
48951 GAGCAAACGG GGACATGTAT CATTCGCCAA GGTTTTCTAGA TAATCCCTGG
49001 TGACCCCTGG CAGGGGATGG TTATCTTGGC GATCCCCAGC CAGGCTTATT
49051 GACTTGCCCC CAGGCAACAC CCAGCAATCC CGCGCCACC CAGGCACTTA
49101 AGCATTGTGT GTAAGCCTCT TTCTGGAAGC TCGCCTTCTG CTTGCCCTTT
49151 GTCTTCCCCA CCCCAGTACT TCTGGCCATT CTCATTGTCA TCACAATGAG
49201 ACAAAGTGGT CCTGGAGACT CAGAACTGC CATGCAGACC TTGAGTTTTT
49251 CTTAGGCCCG GCCAACAGGG TGGAGAATCT TCCATCTCCT AAAGGAGCAG
49301 AACAGACCAG GCATGTAGGA GTTGTGCCCC TGTGCAGGCT GCAGGAGCAG
49351 CTCACAACAA GGCCTGAACA TGGGGTGCTC CCTTGTGTTT CTTTTTTTCC
49401 TGGAGGCTTG GGCTTGCTG GCCAAGGTTG CCCTTCAGGA CAGGGAATCA
49451 GAGCTTTTTG TGGCTGCCTT ACCCAGCCAG GGCAGCACCA GAGAGAATCG
49501 TGGCTGAGGC TTTCTGTGG GCTGCAGTGC CTGCCCTTT AGGGTTTCCA
49551 CAAAACACC TTCCCTGCAA GTAATCCACT GTGTCTGAT TACCAGACGA
49601 GGCTTCTCTA TCATTTGGTG ATTCCAAAGA AAATAATCTA CAGCGGAATG
49651 ACCAAGTTCT AAAACAGGAG CACACAAATA ATCTGTGGAA AGTCTGTTTG
49701 TCATCTAGAT GTTTCGAATA TACACATTTT CCCTTCTTGT TATATTAGT
49751 CGTGCATGAA ACTGATATTA TAATAGATGT GCAATACACT AAAGCTGATT
49801 AAAGGTGAA TTCTTATTCT AAGGTACTTT GTGGTCTCAA ATTTGTCTGT
49851 TCCCACCCCC AGGACTCCCT TAAAACAGAA TAGTTATCAC TGAGAGCAGA
49901 GGTAGAAAAGA AACTAGCTAG GCAGATAGAG CAAAGAGTAC TCAGCGTAAC
49951 ATCCCTTCTA ATGAAAAGCA GCCCCAAAAA TCACATCTCT TTAACAAAGA
50001 GCAACCTGTA AGTTCGGGCT GCAATCATAG ATAAGTAAGA TGGAAGCTTG
50051 TATGGGCAGG GATGGCTGCA GCTTCATGGA TAGAAATGTC CAGCTTGGGC
50101 TAGATACATC CAACATGGGG GCTCCACTCC TCTTTGTAGC ACACGCACCA
50151 TAGGAAAGAG ATAAGCAACT TGGAGTAGCT CAAAAGTCAC GGAGCCTCAG
50201 TGTCCCTTCT GTGGAGCCCA GAACCTGATG CAGGTCTAAG TCCTGTTGTA
50251 TGAACATGTC CTGACCCTGG CGGCCCTGGT GGTGGTGCAG CATAGGAAGT
50301 ATAAGGGATG AGGTCTAGTC ATGGGCCATG GAGCCTTTCT CATTAATCTT
50351 GGCTGTCTGC CTCTAGGGA ATATAATCAA CACTAATAAA GGAGGAAGGT

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50401 GAGCAGCTGG CGCTGTCGCT TTGAGGGAGG ATGGCGATGT GAAAGTCAGT
50451 GACCACCGTG GGGAGGACAC TCCCTGGCTC CATCCTCTGC ATCTTAGATT
50501 TATTGGGACA GTTTGATACA CAGAGAAGGA GGAGACCCAT CCCAATGGAG
50551 GGTTCGATTA GATGAATATA ATCAATGATA AATTCCTAGA GGAGGGACTT
50601 TTTATAATCA ACTCTGAGAA CAGGTTGGAG CTACATGGGA TTGGAGGGGA
50651 GGGTGGAGCC CCTTAAAAGA AAAGCCCCAG AGACTGCCCC TGCCCTCTCT
50701 CTCCCCACA AGTCCATTT ATTATCTTCC ACCCAGGAGC TGTCAGAATC
50751 CTGCCCTTCC GTCTCCAGAT CAAAGTCCTT CAGGAAATGC AACTACTTCA
50801 GTGACAAGAG ATAATTATCA TCTTCTGACA GAGGAGGAAT TTGGGGTTTG
50851 GTCCCACTCC ATGAAGTGGC ACAGTCAGAA TAAAAGGTGA GAGCTTAGGA
50901 GATTAGCGGA GGGTAGAAGA ACACTCTGTC TTGTGACCAG CTTCAGAGAG
50951 CCTGGGGCCA TGGCTTCCTG GTCAACATTA GGCCCTGCTG CATGGTGACC
51001 CCTGGGCAGG CAGTGGGAAG CCTGAGGTGT GGCTCCTGGT GGCCCTCACA
51051 CTGCCACTCT TTCTGGAAGC TCCTATTTGT TCTGTGAGCT AAGCCCCCAT
51101 CCCAGTAGGC CAGCAACACA CTCAAGACCA AGAACAGGCC ATGGTGAATC
51151 TCAGGGCCAC TGAGTGCCTG GGCTGGCAGG GGCAGAGTTC CTCAGGGCTC
51201 AGTGACATTT GGAAGTGGC TGGGCTTTGG AGTCATACAG CTACACTGAG
51251 CTCCCAGCTT CACCGTGATC AGCCCTGTGT CTGGGACAGG GGCCTCACTG
51301 TTCTGGAAC TGAAGCGCCA TAGTCATAAA TTTAACACAC ACTTCTAACT
51351 GCTTTTTCTT TTTTATCTGT CTTTCTCTAT AATCACCATG TACTACTGGT
51401 CTCTTGTTGT TATTAAAATT AATAAACATG TTACACAGTG TGTATTATTC
51451 TTCCTCATGA GTTCTTTACT ATATTCTATG ATTCCACCCA TATGAGGTAC
51501 TTATGTAATT TCATTCATAG AAACCAAAG TAGAAAAGCA GTTAGTTCTT
51551 AGAGGACAAA AGGAAGGTAA AGGGGGATTG TTGTTTAAACA GGAACAGAGT
51601 TTGAGTTTGT CAAAATGAAT AAAATTCCTT GTGAATGTGG ATGATGGTTG
51651 CAGAACAATG TGTGATTAAT TCCTCTGACC TGCACCTTTA AAAATTGTTA
51701 AAATGGTTAA TTTTATGTAT ATTTTACCAC AATGTTAAAA AGGACTTTT
51751 AAAATGAACG GACTATAGAT ATCTGCAACA GCATAAATAA ATATCACAAA
51801 TATAATCTTA CATTTAAAAA TTGATGTAAA AGTATCCATA CTCTGTAATT
51851 TCTTGATTTT AAATCCAAAA ATCAAACTG AGGTTCTGGC TTCCACTAAT
51901 GATGAAGTAG CTAGTTTAAAC TAACAATCTC ACAGAGAAAA ATGATGAATC
51951 CCAGGTAAAA CATTATATGT TATTATAGAA ACACCTCTAT ATATAATAGA
52001 TATATGAAAT ATGTGTGTAT AAAAAGTAA TGCATATTTT AGCTGTGCC
52051 TCCATAGAAG AGAGAAGTAT TGAAGTTAGA AGCCAGCCCA ATTAACACCC
52101 TCTTTAAAGA CAACACTCTT CAAACGGACA AAACAGAATC CAGAGTCTCT
52151 TTAACCTCTT TATACAGTCT CTAGTGCACA ATTTTCCAAT TCAGGAGATG
52201 CGTGAAACA CATGAAATA TAATACATAC ACAAGATAAA AAGCAGGCAG
52251 TAGACATCTC CAAGATGTCC AAGACATAAT CAGCAGACAA GAATTTGAAG
52301 GCAGCTATTA TAAGCATGCT CATGGGGGCA AAGGAAAATA TTCTCATAAA
52351 TGAACAGATG TGAACATCA GCAGAGAAAT GAAAATGAC CACATAGAAA
52401 AATAATAAAA ATAATTGTGA GCTTTTCTAT ATATCAGAAA CAGAAGACAT
52451 AGCAATATAA TTTAACCAAT CTGAGGATAG AAGTAAAAAT AGTTTAAAAG
52501 AAAATGAACA GAGCCTTAGA CCTATCTGTG GGATGATTGA TTCTGAGAAG
52551 AAGAGAGAGA CAGAAAAAAT TAAATGGGGT AGAAAAGCAA ATCAACAAAA
52601 TTTAAAGAAA ATAAACCGAG GCTTAGAGAC CCATGGAATC ATTCAGTCTG
52651 AGAAGGAGAG GAGAGAGTCA GAAGAATTAA AAGGGTTACA AAAATAAATC
52701 AACAATAAAT ATCTGAAAAC TTTCAAAAAT TGTTCAAAAA CCTAATTCTT
52751 TTTTAATCTA AAGATCCACA AACCCCCCAC AAAAATACAA ATAAAACCAT
52801 ACCAAGGCCA TATTGTGATT TAAGAACTA GCAGACAGGA CTTTCAATTG
52851 ACTTGATATG ATTTATTATT TTTACTACTT ATAAGATGG AAATAAGTTC
52901 TCCTTAGTTT TTTTCTTGGG GAAAGTCTGA CATGTGAGGC ACAGATGAGT
52951 TATTAAAGGC AGATGACTTT CCAGCCTTGT CTTAAATGTT CCATTCTTTA
53001 CCTTAGAAAT TATTTAAATT TGTGTCTTCC AAATACTGTA GTAATATTGA
53051 TGCTCCAAAG AGATGTCCCA CGGAGATTCT GCTCTGTGT GTCCACCCTG
53101 CAGGGAGCTG AGGCAGTTTC TTATGACAGT TTCAGAAGCG AGTAGTCGTG
53151 CAGTACTTAA TCTAAAAAAC TTAATGGAAA CATGAATTAA GAGAATGATC
53201 ACTGTTTAGT TCTATCAGCA AACTATTAAA AGTGATCCAA AGGAGGTATT
53251 TATAAGAGA TATTAAGAAG TTTTCAAGG GAGCCTTATT CAGGGCAGAA
53301 ACGCAGACAC TATCGCTGAC CTCACCACAG AAAATACCCT CATGGGTGG
53351 AGGGACCAA GGGACGCTCT GGTCTGCTG ACCTGCATTA ATCAGAGCCA
53401 GGAGGTCCAC ACTAGTACCA TGAGGCCTGG GAAGCAGCCT GCGTGGGGTC
53451 AGAGAAGTGG TGGATGTGGC TCCCAAAGTG GCTTACGGGG TCCCTTCCCT
53501 GTGGCTGTTT CTTACTGGA TGCAGCAGG TCAGGCCCTT CCCCTGTGAC

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53551 GTTTTCTCCT CTTTATCACA GTGGCGGGAG CGTCCCCGTG AGAGGCCCGA
53601 CCCAGGTGTG GGCCACGCTG CGAGCCCAGG GACCAAGCGG CACTCCTGGG
53651 ATGCAGAGGA GGATTTGTGA CAGCTTAGGG AACAGAAAAA ATGGTTTCGA
53701 AAAGGCTAAT GGCAGGTGAC TAAGGACACG ATGTTTTTCAT TACTGGCAGT
53751 GAACTGACGG TTTCATACAC TAACAAGGGG GCTTCTCGAG GGGATCCCAA
53801 GGAGCCCAAG AACTGCCAGG TCGCCCACCA TTACCCCTACG CCTAAGGGAC
53851 AGGCTGCACT GAGCATGTCT GAAACGGTAG GCCCGTTAGC CCCACCCCTA
53901 GGAACGGGTG CACTCCGCAT GTGTAAAAGG GCAGGACCTT TACCCACCG
53951 CTAGGGACGG GCTGCACTAC GCATGTCTGA AAGGGCGTGA CAAGAGGGAG
54001 GAGCAAGAAG GGGCGGGGTG GAGGGGGAGG GGGGCAAGAA AAGGGGCGGG
54051 GTGCGCCCAA CATCCGGCGG AGAAGTATTA CCATGGCAAC CCTCCCGCGC
54101 AGGCCATAAG AGGCAAATGA ACCTTTGTTG GTTGGCGGGA AATCGAGACC
54151 CTGGCAAGGG GGCTTCTCCC TTGAGAAGC CTGAGAACTG CCAGGTCCGC
54201 GGCCGTAAAC CCGCCTTAG GGACGGCCGC ACTGCGCATG TCTGAAAGGG
54251 AACTAGAAAG GGAGGAGCGA GAGAGGGTGG GGCTGAGGAG GAGGCTGTGT
54301 GAGAAAAGGG GCGGGGCGCG CCCAAAGTCT GCGGGAAGAG CGTTACCTG
54351 GCAACCTCTC CGCGGAGGCC GAGAGAGGCC ACCGGCCCTT TGTTGATCTG
54401 CGAGAAATCA AACTACGAAC ACGACAAGCA TTAGCCTGCA GCTCGAGGAG
54451 ACAAGGTGTC ACAATTACAA GGGGAAACTA GCCGCCCTAG CTCCACTGTC
54501 TCCCCAGCAC GAGAGATTG AGAACAGAAA GGCTTCCCTC CGCAGGGCGA
54551 AACTGTGGG CTGCCTGGA GGGCGAGGCA GGGAGCGGAA CCGTCTTCAG
54601 GAAATTTCCG GAGTTCGGG GTCAGGTCCA CTCCCCGGCT GTTGTGTGT
54651 TGTTGGCAGG GCAGAGGGTC TAGGATGCCA GCCTGCTCCG GGCTGCGCTG
54701 TGCGCCTATC CCAGGGCGGG GGGATGCGGG GCGACACCCG CCTCCCGGTG
54751 CATCCAGGAG TTGTAGTCTC TTCACCGGTT CCCCCTGTG GGTGGTGGGG
54801 CTGCAGGAGG ACAATTCAA TTGAGATAGG AGCGGAGGCG GAGCGCGGCC
54851 GTGCAGGGAG GGGCAGGGCG GTGTAGGCGG CTCATTAC CAAGCTTTC
54901 TGGCCATGT TTCCATGCCA AACCTTGCC AAGGGGATTG TCAGGAGAGG
54951 AACTTGAAGG GGAGGCGTGG GCTGGCCAGT GAGGAGGGTG TGTTTTTGCG
55001 AAGTGCGCC CGTCTTTGCC GAAATTAGGA GTGTCTGGTC CTCCTCACG
55051 CGGCTCTCTG CTGCTCAGGT CGATTTTCTC TCCCACCCTC ACCCAGGCTC
55101 TTTCCACAGC ATCACCCCTG CCCCAGCCCC TGGAGCCACC TGCTTTCCCTA
55151 AGTGGTTTTG GAAACTGGGC TGAGGTCCCA AAGGGTGTCC ACTGTGCTGT
55201 TGCTCTCCGC TCTGTCCAAG CAAAGCACAA GCTCAGCCGA CTTTGAAAGA
55251 CACCCACCGC CTGGCCTGGG AATGCACAAG TTCAGAGCTT TGCAAGAAGT
55301 GATCATGGGC TATGGCTTTG TGAATATGTC ACCCTCACCA GTGCCTTTTT
55351 CGCGGACGTG GACGTGGAGG AATGAGGGAG GGTAACTACT GGGCTACCAA
55401 GGTACTGCTA AGAGCAGAAG AGAAAATCCC AGTTTTCAGC CATGTGTCTG
55451 GTTTGACATT TCACCAACCC ATTTAAGTGT GCAGGCCCCC AAATATCTAC
55501 CTAAAGATTA TGATAGTTTA GGCATTTTAC ACTTGAAATT ATTGACCTCA
55551 TATCCACTGA AGCCTGACTG GCCAGTGTCT CAAAGACACA GATGATGACC
55601 TGATCCCTCA GGAACAGCTG GTGCTCCAGC TTTGTGGAGG TGAATTTCAA
55651 GGTATGGATT ACTTGGGGGG TCGTTGAAAC CTGTGAGGCT CAGGAACAGA
55701 TGGTGCTCCA GCTTTGTGGA GATGAATTTT AAGGTATGGA GCACTTGGGG
55751 GGTCTTTGAA ACCTGTCAGG TTTCATATCT CTGCTTTGTG TGAAAAGATC
55801 ATCACCTACA GTAGTCAGGG ATGTGCCCTT ACTTACTGGT GCTCATCTGT
55851 TGAAACTTTA TATCTAGACA ATGGAACAT TGAGGAGCAT TTCTGCTTTC
55901 ATGTAGCCTC TTAATAATTG ACGCCCTAAA GCCCTGTGTC CTCAGGGAGA
55951 GTTCCTTTGA TTCCTGGGTG GTACCAGGTT TCATGCTGTT AAATCTGTAA
56001 AAACCTGCGC GTTAATCTCC ATGAATATAA GACCTGTGTC TTTCTTAAAT
56051 GCCCAATTT TTTCTTCTCT TGTCTTATAT TCTGAGCAGG ATTTCAAATA
56101 CTGTATGTAA GGAAGTAGTG AGAGTGGGCA TCTTTATCTT AAAATAAATC
56151 TTAGAAAAGA TTTCAACATT TCACCACTGA CAATGTTAGC TATGGGCTTG
56201 TCCTATAGCT AATAAAGAAC GCATCTCTTT ATTTTGAGGT ATATTCTTTC
56251 TATACCTAAT TTGCTATAAA TTTTGTTAGG AATGGATTTT AAATTTGTG
56301 AAAATAATTT TAGGCATGCA TAAAAAGTCA TGATTTTAA TCTTTTGTG
56351 GTGTAAATAA GGTGTATAGC ATTTATTGAT TTCCACATAT TAAATATTA
56401 TTGCATCCCA GGAATAAATC CAACTTGATC ATAACATCCA ACTGTGTTGC
56451 CCAGGCTAGT CTCAAACCTC TGGATTCAAG AGCCCTCTC CTCTCAGCCT
56501 ACGAAAGTGC TGGGATTAAA GGTGAGATCC ACTATGCCTG GCCATATATA
56551 TATATAATTT GTAAATAAAA ATAACCTTAT ATACAAGGAT AAATTCAAAT
56601 GTCCACGGTG AGGTCTGGGC TTCAGCATAA GGAGGAAGTC TTGCCTGAAA
56651 AGGGCTGCAG CTTGGAACCT TTTACCCTGT CGTCATGTGG CTATGAGTTG

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56701 GTTCACATCT TCTGTCATTC AGGACCCGAA GGGGTGGGAC CTGGGGCCCT
56751 ATTATCACTG GTGCTGGGGT AAAAAGTGTG TTAAAGTATG CATTTTAATG
56801 CTTAGCAATG TTAATTTTTA GTGAGAAACA AGATTACTTA ATTTAATATA
56851 ACCAGATTTT AAGTTACTAA AAAAAACCC TAAAGTTATG ACACAGGTAT
56901 TTCCTCTAAT GTTTTTTTGG GGGGTTTCAA GTACCTATGT CATATACTGA
56951 AACCTACTGT TCTGTAAGCC CTACCCTTAA AACAATCTTG TTGTTATTGT
57001 GAACAGTTAC TTAGTGTAAG TCCTACCCTT AGGCAAATTT ATATGGTGAT
57051 TTCAATTGTG CTTACATTC CTTTCCTGTG TTAAGTGTCT GGGTTTAGGG
57101 GTTAACAGTG GGAGGATCCA CTCATCTTCA GCCATCTGAG ACATAGCTTC
57151 TATTCATAAG TCCATCTTAA ATGTTCCCTT CTGAGAAACT TGATTTGTCA
57201 GCCTCATTCT TCAACCTTTC AACTCCCTTG GCTTTTAAAG GCAGGTTTAC
57251 ATATACCTAC TCACAACAAA ACACCCTCAT ATATATGGGC TGTCAAATTC
57301 TATAACATTT TTATGTGGTT CAAGACTGTA ATGTGTAGCA CATGTAGTTT
57351 TGTATATGGA TAGTATATTT TATATAGTAT ATTTTATATA GCTACTTTAT
57401 ATTACACATC ACTAAAATAC ATGTTCAAGTA AGTGCTCACT TAACGTCATT
57451 GATAGGTCCT TATAAACTGA CTTTAAAGTAA AAAAAATAC TGTGTGCCAT
57501 GGAAAATTAA CTTGTGTATA TCAATTAGCC AATGGGAAAA TTGGGTTTAT
57551 TATATAGTAT ATTGTGTTAC TTAAAGTCAC AGTTTCCCAG AATCTATCAA
57601 AAAAGTGAGA ACATACTGTC ATTAGTATTA TGTAAGTACAT TACAGAATTA
57651 CACTGTTATG GTATGTTATT GTAGTCTTAG CAGTTGGTAG TATAATGTGT
57701 TTCAGTTTCC CCCAAGGTCA CAGAATTATC CAGGCCAACC AATAACACCT
57751 CCTGTGGGAA CCAGGAGCAT CTCACCCTCT TGATACTACA AAGCCTTCCC
57801 CGACACCTCC TGTTTGTCT CTCTGCTCCC AGGTGCAATG GCTGTGTGGG
57851 TCTGTATACC TTACATAGCT TTCTCCTTCC ATGATTATAT GTAATGAATA
57901 ACTGCTGTCA ATCTCATCTG TCCAGTGATT GGTGCCATGG TTTTAACTAT
57951 TCCAGTAGCA TTAGGGTGGT AATTTCTCCC TCACCAATGG GGTAAGGGG
58001 AGGCTAATCA AACAAATCAC AACACTAATG GGATTAATCA CCCATGACGG
58051 AGGACATCTG CTCAACTTTA ACTGCTTTTG GCCTACTGGT TTCATGATAC
58101 ATTAAAAGTC ATCTCTGTCA GAGCCATCAG TTTGTGGTGG GCTTTTGCTT
58151 TGGTCTAAAT AACAAATTTG GGCCTTTATC ATGATTGGCC TTCCCTGCCC
58201 AACTAAAGC ACACATTACC TAGACATAAA TATTCAATGG ACTCTTCTCC
58251 CGCGTGACGT GTCATCATGT TTAGCCTGTG TTTGGCAGGC AGTTTGCAAG
58301 AACTTGCCTG GTCAGGCAG TGAAAAACACA GCACNNNNNN NNNNNNNNNN
58351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNGGCAGG GAAAACACAG
58451 CACCTTAATC AGTCAGCACT TCAGGCGGGA TTACCACAAG AACGGCCATA
58501 TACCTGTGGT CGCTTCATCT GGTCTGCTTA CTATTACTAA ATGCCTGGGT
58551 AGTCATCTGA ACGTTGTTTA TTATTGCACA CTCTCAGGAC AGACCCAGGG
58601 ATGGTCTTCT GTAAATTTGC AAAACAAAAA GGGACTTTTA CTTTGGAGAG
58651 AATTATGCTT GTCATTCACT TGCTCTAAGA AGTGCTACTG TCATGCAAGC
58701 AAGAACAGTG GCCTTGCTTT TTCTGAGCTG CTGCTTCTCT TGCTGCTGTC
58751 ACGTGCAATC TCATGATGAG GTGTGCATTC CTTGTGCCTT ATGGCTTAGG
58801 CACTGATGAG TCATAAAAAG GAGAAAGAGA ATTTAATATT AGTCCCTCCC
58851 AAAACATTTG GGGTAATTTCT CTCACTGTAA AACCCCTACT CATCATGTGA
58901 ACTTTTAGCA CTGCTGCTTA CCAGTATGCC AATGGTGCAA TCTTAGGATC
58951 AGAAGTTTGA TGGACTCAAA AAAAAAAGAA AGTACCATAA CGAATATGGG
59001 TGCTAATCCC AGTGAGATGG AGAGGCAGTA AACACCTTCT TCCAAAGAGA
59051 AGACAGATTG CAAATAAACA AATAATGATA TAACTCAAGA AACTAGAAGA
59101 GGGAGAACTT ATCCCAAAGT TAGCAGATGA TGAAATTAAT TAAAAAACA
59151 GAGCAGAAAT AAATACAATG AACACTAGAA AAAAAAACA GAAATGTAG
59201 AAAAAATGTA AGAAGTTGTT TTTTTTTTGA AAACATAAAA TCTTCCTATC
59251 TTTAGCTAGG CTAAGAAATA AATGCTCAAA TAAATAAAT TAGAATTAAT
59301 TGGAAGATAT TACAAGTGGC AAAACAGACA TACAAAAGGT CATAAGATTG
59351 CTGTGTACAT AGACTCCTAT TTACAATGAT ATCCAAACAA ATTGTGTAAG
59401 GGAGAAGACA TGAATAAAT TCTAGACATG TACCACCTAC CAAGACTGAG
59451 CCATAAAGAA ATAGAAAACA TGAATAGATC AGTAATGAGT AAAGAGTTTA
59501 GATCTGATGA CTTTACTCCT GAATTTTACC AAACATTTAA AAAGAACCAA
59551 ATCTTTGAAA AAAAATTGAA GAAACAGGAA TACTTCCAAA CTCATTTTAC
59601 GAAGCCAGCA TTACCCTGAT ACAAACCA GAGATAGACA TTACAAAAAA
59651 AAAAAATTACA CGCCAATATC CCTGATGAAC ATAGATGCAA AATCATCCAC
59701 AACATAGTTG CAAATGAAAT TCAAAGCAC TTTAAAAGGA TAATTTATTT
59751 GATGTGGGTG CCCCCATCC CACCTTTTCT TAAAAAATGA AAAAAAATA
59801 GCATGGCATG GTCATACATG TCTGTGGTCC TACCTACTTG GGAGGCAGAG

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59851 GTGGGAGGGA CACTTGATCC TGGGAGGTAG AGGTTGCTGT GAGCTGAGAT
59901 CAGGCCACTG CACTGCAGCC TGGGTGACAG AACAAGATCC TCTCTCTCTT
59951 TCCCCCACTT TGTGTGTGTG TGTGTCACAC ACAAAGGGGA GGGGTGAGGG
60001 TGTGGATGTG TGTGTATTAT TCAAAATGAA AACAATGACA ATTATTTTTG
60051 TGTACATTTA TATTTTTTGG AGAAAGAGTA TCACTCTGTC ACCCAGGCTC
60101 AAGTACAGTG GTGTGATCTT GGCTCACGGC AACCTGTGCC CCCTAGGTTT
60151 AAGCGATTCT TCTGCCTCAG CCTCCCAAGT AGCTGGGATA CAGGTGCCCA
60201 CCATCTTGCC AAGCTAATTT TTGTATTTTT AGTACAGACA TTGTTTCGCC
60251 ATGTTGGCCA GGCTGGTTTT AAACCTCCTGA GCTCAAGTGA TCACCCACTT
60301 CAGCCTCCCA AAGTGCTGGG ATAACAGGCG TGAGCCACCG TGCCTGACCA
60351 ATGACAATTA TTTTAAATTT TTAGATTTTA CAATCTTTCT CTCCTCTTGA
60401 ATTTGAGGCA GCCTGAGCTT TGAAAACCTGG CAATCTTCTA TTGCAGCAAT
60451 GTGCAGTAGA AATAAAATGT GAGCCACGTG TGTCAAAGTT TTCTAGTAGC
60501 AGCATAAAGA AAAAGAAATA TGAGTGAAAT TGATTTTAAAT AACTTAGCCT
60551 AATATATCCA AATATTTTTA ACATATAATT AGAATGAAAT CATTACATAT
60601 ATATAGATAG ATATAGATAT AGATATATAT GTAACATAAT CTCTAAAATA
60651 CTTTCTGATA TTTTCCCTA GCATATCTCA GTACATACTG TGTACAATTT
60701 GGGTGCTCAG TAGCCTGTTG TGGCCAGTGG CTGCCACATT GCATGTGCAT
60751 CTCTGAGGGC TCTTGACTTT TCTGACCTTC GGGAGGTAAA GGGCCTGAAT
60801 TTTCTTTTTC TGCCAGATAG GAGTGAATGC CTCTTCTCTG CCAATATCAC
60851 TCCTGTTTCA AGGTAAAGAG AGGTGGTGCA CTGAGAGACA GGAGGGACCT
60901 ACAGGAAACA AGTGTCCACA GATAGACCAC TGCTGTCCGC TGCTGCTTGG
60951 TGTGGACTCA TCACTCTTCC AGAAATCAGA CAGAAGTCCA AAAAATGGGG
61001 ACCCAGAAGG GGGAAACCTC ATGTTTTTAG ATCTGTCCAT AGCCTTAATC
61051 TCCAGAAATT AGATGTCAAG AGACTAGATT AAAGGCAAAC CTTTTATCTT
61101 GCAATTTGGC TTTGGCAAT TAAATAGAA ATAGAAATGT GTCACTATAA
61151 AAATCAATTA TATACAAAGG AAGGCAATAA GAGCAGAAAA GAGGAGAAAA
61201 TACCTACGAG AAACAAATAG AACTATTAAC AAAAAGGAAA TATTCCATTC
61251 TTTTCAGAAT TAAATGAAT ATATACATGG AGTGAAATAT ACACTGGAAA
61301 TATGTAAATT GGCTAAAGAG ATTTTAAAAA AACAAGATTT ATTTTCTGTT
61351 GTCTATAAGA AACTCAATTT ACATCTAAGC ACACAGATAG GCTAAAAGTG
61401 CCAGTATGAA AAATACCTTC TAGGAAAAC TCAATCAAAT GACAGCAACG
61451 TGGATCATAA TTATGCAAAA TACACATTAA GTCAGAACTG AAACAACAGA
61501 CAAAGAAAAG TGTTGTATAA TGATAAAACT GTCAATTCAC TGGGGAAGCT
61551 GTGTTAATAA TAAATATGTG CACACTTCAC ATCAGGGTTC CCAAATGTAT
61601 AAAGTTAACA TTGACACAAA TGAAGAAGGA AATGGCTATG CAAAAATAGT
61651 AAGAGACATA ATTACCCAC TACCCACTAT CAGTAATGAA TAATAAAGCC
61701 AGACAGAAAG TTAACCTGAG AACAGAGAAT TTGAATAACA CTGCAAACCT
61751 TAAACCTAAC AGACATATAG AAAACACTAG TCACAGTGAA TAGAAGTGAA
61801 AAAACAAAAG AAACAAACAC TCCACACAGC AATATCAGAA TATACAATTT
61851 TTTCAATAGG TCATGAAACA TTCTCCTGGG TTGATGACCT ACTAGGACAC
61901 AAAACAAGTT TTGCTAAATT TTAATATGGT AAAATATGGG CCAGGGATGG
61951 TGGCTCATGT CTATCATTC AGCATGTTGG GAGGCTGAAT TGGGAGGATT
62001 GAGTGAGTTT AGGAGTTCAT GGCCAGCCTG GGCAACATAA GGAGACCTTG
62051 TCTTTACAAA ATATAAAATT AAAAAATTAA CTGGGCATGA TTACACGTGC
62101 CTGTGTGTCC AGCCACTCAG CAGGCTGAGG TGGGAGGATT GCTTGAGCCT
62151 GGGAGATCAA GGCTGTGGTT AGCCATAATT GAGTCACTGT GCTTCAGCCT
62201 GAGTAACATA GCAAATCTCT GTCCCAAAAG AGATTAAAT ATTACAACT
62251 ATCATTTTTG ATTAAGAGG AATACAATGA GAAATCAATA GCAGAAAAAA
62301 TACTGGAAAA TCTACAAATA TGTGGAAATT AAACAACCCA CTCTTCAGCA
62351 TGCTCTCGTT AAGGGTCGGA AGACAATATT GTGAAGATGT TCACACTACC
62401 CAAAATTATC TACAGATTCA ATGTGATCGC TGTCAAATTT TAACTGTCAT
62451 TTCATTTGCA GAAATACAAA AAAAAATCTA AAGCTTATAT GGAATCTAAA
62501 GTGAGTATCA AGAGCCAAAC AACTTTCTAA AAGCATAATA TTGGAGCTAT
62551 GACACTCCTT GACTTCCTAA TGTATTACAA AACTACAGTA ACCAAACTAT
62601 TTGCTACTGA CATAAAGGCA GACAGACAGA CCAATGGAAC AGAATAGATC
62651 ACAGGAATAA ACTGTCATAT ATATGGCCAA ATGAGGAGTT ATTTTATAT
62701 CCATATTCAT TGCAGCATTA TTCACAACAG CTGATAGGTG GAAGGAACCC
62751 AAATGTCCCT CAGTGAATGA GTGGATAAAG GCAATTTGGA ATATACAAAT
62801 AATGGAATAT TATTCAGTTT TTTAAAAGCA GGAGATCTGA TTATTTTAC
62851 ACTAAGAATA AATCTTGAGG ACATTATGTA AATGAAATAA ACCAGTCACA
62901 AAAGGACAGA CACTGTTTGA CTCCAGTTAA ATAAATATC TAATGTAGTT
62951 AAACCTTTAG AAACAGAAAG TAGAATAGTA TCAGTCAGAG CCTTAGGGGT

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63001 GGAAATAAAA GGGTAGTTGT TGTTCATAG GTATTGAATT TTAGTTTTAC
63051 AACATAAAAT CATTTTAGCG ATATGTTGCA TAGCAATGTG AATATATTTA
63101 ATATTATTTA ACTATGTACT TAATATATTT AAGATGGTAC ATTTTATGTG
63151 TTTTGAGTAC ATTA AAAAATG AAAA ACTTTC TAAAGAGATA CATATTTATA
63201 ACCTTTTTCA AAAATTACCT CCAAATCATA AAAATGTCAG AAAACAATA
63251 AAGAGGCCAG GTGCAGTGGC TCATCCATGT AATTGAAATA CAACAGGAGG
63301 CTGAGGATGG AGAATAGCTT GAGGCCAAAA GTTGGAGACC AGCCTGGGCA
63351 ACATAATAAG ACCTCATCTA CAAATCACAA GCAAAAGGAA ACTGGCAAAT
63401 TAAAAAATAT GTGAGACTTA AAACAGCAGA CTCTTGACGG CTCAAAAAAT
63451 TTAATATTAT TAAGATGTCA ATACTACTCA CAGTGAAACA CAAATTCAAA
63501 GTATTTTCTA TCAAAATCCC AATGTTACGA TTTTTTTAGA AATATTATTT
63551 TAAGTCTTAA AATTCTTACG GAATATCAAG GGACAATGAG TAGCCAAAGA
63601 AGCTTTAGAG AACGAAGTTA GAGGTGTCAC ACTTCCTGAT TTCCAAACAG
63651 ATTACAAAGC TATAGAAATA CAACCAGAAA GACAAATAGA TGATGGAAACA
63701 GAATAGAGAA CCCAGATATA GACCATCATG AATATCATCA GATAATCTTC
63751 AAACAAGTTG CCATTACCAA ACAACAGGGA AATAACAGAC CCTTTAACAA
63801 ATAGTGTCTT AAAAGTGAAC ATCAAAATGG AAGAAAATGA AATTGGACTT
63851 CTGACTTGAA CCATATACAA AAATATCTTA AATAAATTAA ACAAATGTAA
63901 GTAAGATAGC TATAAAACTC TAAAAATATG AGGTAAAAAT CATGACATTT
63951 GTCTTGTTAA TTTTTTAAAA TATGACATTA AAAGCAGAAG TAACAAGAAA
64001 AAAAGCAGAA AAATGGGACT ACCTCAAATG TAGTAAGCTT TCTGGACATA
64051 AAGGAAACAT TTAATGTCAC GTAAGAAATG AGAAAAAAT TACAAATGAT
64101 ATATTTGATA GAAGTTAATA ACCAGAATGT ATAAACAAC TTAAACTCA
64151 ACAAAAAAAA CTGAACAACC CTATTTAAAA ATGGGC AAAA CTCTCAACAG
64201 ATGTTTCTAC AAAAGAGATA TACAAATGGC CAAGAGGAAT TTGAAAGGAT
64251 GGTCAAATTC ACGAATCTTT AGAGAAATGA AAAGCAAAAT CCCAATGAGA
64301 TATTACTTCA CACTCATTAG GATGGCCACT ATCAAACGAG AGAAAAATAT
64351 AAATATTTTC AAGGATGTAG ATAAATTGAT ATACTTGTGC ACTGAGTGGT
64401 GGAAAAATAA TAATGCAGCC ATTATGAAAA ATAGTACAGA GGTTCCCTCAG
64451 ATATTAAAAA TGGAATTATT GTACTATCTT GTTGGAGGTC AAAAGAATGA
64501 GTGTTGTGAC CAACTCATTA TACCACTGGA GGCTATATGA GCAAACAGCA
64551 AACTGTTCTC ATGAATGCAG GATGTTGGCA AGCTGACAAC TGCATCTGCA
64601 ACCAGAAGGA ATGCTGAGGG CAGTCATGCC CCAGGCACAG TGTTTCTTGT
64651 GGTATCTAT AGGAACATCT GGAGCCTGTT GTACAAAGAA ACCAATTATG
64701 TGAGCCTGTG ATAAATCAGG CAGCTGACTA ACCATTACCT GCTTCCTGCC
64751 CTGTTGATTC TACCTAATGA ATACAAAGGG CTGTATAAGC TCAGGGCCCT
64801 TGTTCCCTAT AAGCAAGGAG CCCCCTGACC CCTTCTTTAA AACAGATCTT
64851 TTTGTCTTTG TCTTCATTTT TGCGTTTGTC CTCTTCTTTC AGTCCTGAAC
64901 TGACAGCCAC AAGTGGCACC TGAACAGGGA CTTGAACAAA GAAGGTCTGC
64951 TGGAGCAGAA AAAGTGAAC TGACCAGATG AATGAGAAAC CCTGGGATGA
65001 GTCTGCCTGC AGAGGATATA AGGTCAAGT CTTAAAGAGG TACTGGGAGT
65051 GGGAAAGTTT TGAATCAGGG TAACGTGGGG GCAGAGTTTG TCTGTTGAGG
65101 AGCAGCATTA CGTGCAGTTG CTTAAAGTTT TACGTAAACA ATCTGGTGCT
65151 CAGGTTAGTT CTCAAACGCT GACTAAGCTG CTGCAGGAGG TTATCATGCA
65201 TAACCCCTCG TTTCCGCAGA CAGGCCTCTT TGATGTGGAA AATTGGAAC T
65251 GAGTAGGGGA AGGATTA AAA TGGGCTCATC AAAAAGGTCT TAAAGTTTAT
65301 CCTTCCTTTT TTTTCTGTTT GGAGTTTAGT CCATACTGTC CTCTGCCAT
65351 TATCTCATTC TTATTCTGCC AAACCGCAGG AGCCATGTTT TGAATCTCAA
65401 ATTTTGAAAG AATCTTTTGT CCCACCCACA ACACCCAAAG AAAATAATAA
65451 ACAGGAGAGG GAGGATGAAA ATTGGCGTCT ACCACCCCTT CCAGTAGCAG
65501 AAACACCTGT ACCATCTCCT TCAGTAACAG AAATAGAGAC CCCACTGCAA
65551 AGAATTCGCG GGA CTGTAC CATAGCTGGA GAGCCCTTAG GACATTGCAC
65601 TTTCACTATT TCTGTAAGGC CTGATCCAAA TAATCCACAG CAGTTTATTT
65651 ATGAACATGC CTCACTAGAG TTTAAGTTGT TGAAGGAATT AAAAGCTAGT
65701 GTAGTGAATA ATGGAGTACA GAGCCCATTT ACTTTAGGAT TGTTAGAATC
65751 TGTATTTTGA ACTATGTGTC TTCCATCCTT TGATGTAAAG CATTTGGCTC
65801 AACTTGTGTT GTCTGCTAGT GCATATCTGA AATGGAAATTT AAATTGGCAA
65851 GAACTGTGTG CACACCAGGC TAGCACAGAA TTGTGCTGCC GGGCACAGGG
65901 GACATTACAG AGGATATGCT GTTGGGTAAT GGCCCTTATT CAGACCTGGA
65951 ATATCAAATG ACACTCCAG ACGCTGCTTA TAAGCAGCGT GCACTGGCTG
66001 CTAAATGCAC CTGGGCCACA ATTCCAGAGG AAGGGGTCCC AATACAATCC
66051 TTTTACATG GCATGCAAGG GTCAAAGGAG CACTATGCAC ATTTTCTTGC
66101 ATGATTACAA GAGGCAGTGA GGCATCAGAT TCCTCATACC ACTGCTGCAG

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66151 AAATGCTAAC CTTAACTTTA GCTTTTGGAGA ATGCAAACAC GGATTATAAA
66201 TGTGCACTGG CTCCTGTGAG ATGTACTAAA AACTTAGGAC ATTTTCTCAA
66251 AACTTGTCAA GATGTGAGAA CTGAGCTTCA TTGCTCTACA ATGTTAGCTC
66301 AAGCAATGGC TAATTTAGTA GTTAACAAAT CTA AAAAGGG CTAAGGGTCA
66351 AACCTAAAA TGGGAAAATC TTATAATTGT GGAAAAATCG GACATTTCAA
66401 AAAGGAATGC CATCAGACCT TGGGCAAAAG GGATCTTATA ATGCAATACC
66451 CAACCTTCAG CAGAAAAAAT TCCAGAAAT TGCCCTTGT GCAATAAAGG
66501 AAATCATTGG ACTAATCAAT GCAGTTCAAA ATTTTCATCAG AATGGCACCC
66551 CTCTGTGCGG AACCAAGAAG GGAGCCTGGA CCCGGTCCCC TCAAACAATG
66601 AGGGCATTTC CTGTCCAGGC CACAACCCCA TTTCAGGGAG GAGTCTATGG
66651 AGGAACATTG ATTCCCTTTC CCCAGGAACA CCCAGAAGCA CAGGAAATAG
66701 ATCTCCCTGT CAGAGAATGG GTTACATTAG TTGGAGGAAA CAAACCCACT
66751 AAAATPCCCA CTGGTATTTG GAGACCTTTG CCAACAGGAT ATATGGGATT
66801 AATTTTGGGT AAAATCCATC TCAACTTACA GGACATTACT GTAGTCCCAG
66851 GAGTTTGTGA CTGTGATTAT GAAGGAGAAA TTCAAGTAGT GGTAATATCA
66901 CAAGATTTGT TAGTTTTTGA ACCTGGAGAA TATGTAATC AACTACTGCT
66951 TATTCCTGG GAGTGTGTTT CTCTCCACA TAAGGAGAAA TGAGAGAATC
67001 AAGGATTTGG GAGTACAGCT AGGAGGAAAA TTTATTTATC ACAACCCATA
67051 GCATCTAATA GACCCACCTG TACAGTGCAA ATTAACGGAA AAAAATTTCT
67101 ATGGGCTTAT GGATATGGGA GCTGATGTGT CAGTAATATC TAAAAACAAT
67151 TGGCCCCCAT CTGGCCCTT GCAATTAACCT CCTACATCGC TAGTGGGAAT
67201 AGGAACAGCT CAAAGTGTTT AACAGAGTGC TGAAATTTTA CCCTGTCTCA
67251 AACCAGATGG ACAGTCATGT ACTTTTAAAA TTTATTTTGC AAATGTAACT
67301 GTTAACCTAT GGGGCCAAGA TTTACTTACA GCATGGGATA TAAGACTTGC
67351 AAATGAAACT ATTGACAATC CAGGGTTCAA AATGTTAAAG AAAATGGGAT
67401 GTCAGGCAGA AAAGGCTTAG AAAAGTCCCT ACAGGGAAAC ACTGATCCTA
67451 TATCAATAGC TGGGCAAAAC GATAGAAAAG GGCTAGGTCA TCAGAATTTT
67501 TGATGGGAGT CACTGATATT TCTCCCCAT CTACTGTTTT ACCGCTGGAG
67551 TGGCTGACTA AAAAACCTGT ATGGGTGGAT CAGTGGCCCC TATCACAGGA
67601 GAAACTAACA CAATTCATC AGCTAGTAAA AGAGCAAATG GATGCAGGAC
67651 ATATTGAAGA GTCAGTTAGC ACCTGGAATT CATCAGTATT TGTAATTCCT
67701 AAAAAGTCAG GAAAATGATG ACTGCTACAT GATTTGAGAG CTATTAATGC
67751 ACACATTAAA CCAATGGGTG CATTACAGCA AGGTCTGCCA TCCCCGGCAG
67801 CCTTTCCAGG AGGCTGGCCT CTCAAAGTAA TATATCTTAA AGATTTTTTTA
67851 TTTATTTTTT TATTTTACTG TTACATGAGC AGGATAAGCA TCGATTTGCC
67901 TTTTATGTGC TTTCTGTAA TCAAAAAGAG CCTGTCTCTC ATTATCAATG
67951 GAAAGTCTTA CCCCAGGCA TGCTTAACAG CATTATATCA GCATGTTGTA
68001 GGATAGGCAT TAAAGGTGCC TCTGAATATG TTTCCACAG CCTACATCCG
68051 TCATTATATG GATGATATTC TTTCTGCCCC TCCTACAGAT CAAATTTTAT
68101 ATCAGTTATT CAGATAAATA AAATGAGCTT TGACTTAAAT GGAATCTCAA
68151 AATAGCTCCA GAAAAGGTGC AAACAACCTC CTGATACCAG TACTTAGGCA
68201 CTATTGTTAC TGAAAGAAGT GTTTGGCCTC AGAAAGTAGT CCTCCATAGG
68251 GACAGATTAC AAACTTTGAA TGATTTCCAA AAATTATTAG GGGACATTAA
68301 CTGGCTGTGC CCAATGCTAG GTATTCCTGC TTATCAACTC AAACACCTTT
68351 ATCAGACCCT TCAAGGAGAT TCTCCATTAG ACTCTCCTCA GCAACTTACT
68401 AAGGAGGCAA AAGCTAAGTT ACAACTTGTA GAGCTGATGT TTTGGCAACG
68451 ACATGCCCTCC TGGCTACAGC CACAAAAGGC TTTGCTTCTG TTTATTCTTC
68501 CTACCCCCCA TTCAGCAACA AGACTTTTAG GCCAATTCAT AGTCAAATCT
68551 GTAGTAGTAT TAGAATGGCT TTTTTTAAAT CCAATCAGAC AGTGAAATCT
68601 TTGCAAGTTT ATCTTTCTTT AATTACTCAA CTTATAACAA TAGGTAGGCA
68651 TAGATCAAAA ATGCTTATGG GATATGATCC AGACAAAATT ATTGTTCCCT
68701 TGGATTCCCA ACAACACACT GCAGCATGGG AAATGTTGAC TGCATGGCAA
68751 ATTGCTCTTG CAGATTTTCAT AGGAATAATA GATAACCATT ATCCATCAGA
68801 CAAAATTTTG CAATTTTATA AAGTTCACCC TTTTATTCTC CCTGTAATCA
68851 CTCATCACAA GCCTATTCCA GGTGAACAGA CCTATTTTAC TGATGGTTCT
68901 GCCAAAGGAC ACGCAGCTAT TTATGGACCT AACATACTTA GACAATAAAG
68951 ACCTCTGGAG CTTCAGCTCA ATGCTCAGAA TTAATGATAG TTATTCAGGT
69001 TTTACAGCTC ACCACTTCAT CTCCTAATAA CATTGTTTGT GATTACGCCT
69051 ATGTTGTAAA TGTAGCCAGT CGTGCTGAAA CTGCCACTAT TAAGAGCACC
69101 CTAGAACCAG AGCTGCTTAA CTGTTTCTA AGACTTCAAC AAGCTGTTCTG
69151 CTCTCATGCT ACTCCTTTTC ATATTTCTCA TATTCATCT CACACGCAAC
69201 TTCTGGACC ACTATCTCTA GGTAATGATA AAGCAGATA ACTAATCGGT
69251 TCTGTATTTT AACAAGCCCA AGCTTCTCAT GCATTACTGC ATCAAAACAC

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69301	CTCTGCCCTT	ACTCGTATGT	TTCATCTGCC	TCATGGACAG	GCTGCAGCTA
69351	TTGTGCAAA	CTGCCCCACT	TGCCAGCATG	TTCCTGGTGT	TGCACCTGTG
69401	GAAGGATGTA	ACCCACGAGG	CTTGGCACCA	AATGAAATCT	GGCAGATGGA
69451	TGTTACACAT	ATAGCAGCCT	TTGGGAAACT	CAGCTGTGTT	CGTGTGACTA
69501	TAGACACTCC	CATATGCTAC	ATGTCACATG	CCAAACAGGA	AACAGCTGGC
69551	CATGTCCAAC	AACATTGTTT	GTCATCATTC	GCCCATATGG	GGGTCCCTAA
69601	ACAATTAAAA	ACTGACAATG	GACCTGCTTG	TGTTAGTCAT	GCTTTTCAAA
69651	ATTTTTTACA	GTTGTGGGCA	ATCACTCATA	ACACAGGAAT	TTCTTACAAT
69701	TCTCGAGGAC	AAGGCATTAT	AGAGTGGGCA	CATCAAACAC	TACAGTGTAT
69751	GTTGTAAAAA	CAAAAAGGGG	GAATAGGAGA	CAAGCTACCA	CCTCAAACAA
69801	AATTACATTT	ATCCTTATTT	ACTTTTAATT	TTTTACTTTT	GATATGGATA
69851	GTAAGACTCT	GGCCAAACAA	CATTGGCAAA	TGTTAGAGGG	AAAGAGGAAA
69901	GTTTACCCAA	AGGTACTATG	GAAATCCCCA	GAAGAAGGAC	AATGGAAAGG
69951	CCTGGTGGAT	TTACTGACGT	GGGGATGAGG	GTATGCTTGT	GTTTTTTACAG
70001	GAGATGGATA	AACCGTGTGA	GTGCCCTCAA	GTTGTGTGCG	ACCATGGAAT
70051	GGGAGACTGG	AGGGATACAT	GGATCCCAAC	TACAGGCCCA	GCTCCTCCAG
70101	TATGAGCCAT	GAGCCAGTTG	AATCTGAATG	TGAAGATGGA	ATGAAGACCG
70151	ACGAGAGTCA	CACTGACGTC	AACCCTCATA	ACATGGGGTC	AGATCAAGAA
70201	AACCACACCA	GAAGCTGAGA	AACTGGTGTA	GTGCCAGGGT	CAGGCAAAAA
70251	CCCCTGACTC	CATGTTTATG	GCCATGCTAG	CTGTAATATC	CTGTGCAGTA
70301	TGATTTTCT	GTGCAGAAGC	AAAAACATAT	TGGGCATATT	TTCTTAACCC
70351	ACCGGTAGTG	TGATCATACT	CTGAAGCAGC	ACTCCTCCTG	AGATATATCA
70401	TGATCAAGGA	GCATCAGTAC	CAGGACCTCT	AACTCCCCCT	GACACAGAGC
70451	AATTAGACTC	TCATAACAAT	GGTATCAATT	ATACCACTCC	ATTGGAGGGA
70501	CTTCCTTTAT	GTGTCACCCA	GGATACATTG	CTCAACTGCA	GTTGCCTTGC
70551	AGTTTGATCC	CAAGCATGGT	TGAGTTACCA	TAAAAAAATT	ATGTACCTAT
70601	TAGACCTTAG	CTTTATTAAT	ATTACTTGTG	TAGTTACTAA	TCACTCCTGG
70651	CCCCATCAC	CAAATTGTAC	TGATTATACA	GAATGGGCTC	CCTTTGATAA
70701	TTCTCACCCC	CCTCCTTGGG	CCCACTGTCT	TGGCCCCCTA	GCTAGACAAT
70751	AGTCCATGTT	AATGGGAGAC	ATTATTGACT	GGGTCCCTG	TGGTCATTAA
70801	GATGGGAGAG	ATGAGAATCA	GACCACATGG	CATAAACTTC	ACTGGCACTG
70851	GTGGCGAAAC	TTTAACATCT	CTTCACTTCA	ACACACTGGG	ATTCAATCCC
70901	AATCTGCCAT	GCAACTTGCT	TGGCATGGAA	CGGGCTTTAG	CCCACCTTTG
70951	CCTCAATGGC	ATTATCAAGG	AAAGAGAGGT	CCAATTACAG	AGTCTATGTG
71001	GAAGGCAGCA	CTCCCATATA	TGAATGGCAG	CATTTGGGTT	GGGACACTAT
71051	CCAATAATAG	TAATAGTGCT	CAATACAGTT	TAATGTTACC	TTTGTAAGAA
71101	ATGTTTGAAA	TTTGTGTTTT	TAATCCCTAT	GTTTTTCTAG	CAGCAAAAAA
71151	GGACCAACTC	CAGGTAAACA	ATGCCCAATT	GAATTGTGAT	TCCTGTCAAC
71201	TCTATCATTG	CCTTAATCAT	AGCACAATAC	AAACACACAG	CATATCCACC
71251	CTAATAATTC	TAGGTCGCAT	TCCTGGATTA	TGGATTCCCTG	TAAATCTATC
71301	TGAGCCTTGG	GCAGCCACCC	CCACTTTACA	TTTTGTAAAA	CTTCTTACTC
71351	AGCTTACTCA	TGGCACTCGT	AGAGCCTTAG	GCATGATAAT	TTTTACTATA
71401	GTCTCCTTAA	TTACATTAAT	ACCCTCTGTT	GTGGTGTCCCT	CAGTAGCACT
71451	GGACAGCTCC	ACTCAAACAG	CTCAATATGC	AGAAAATTGG	ATGCATACAG
71501	CTGACCAGGC	ATGGATGTTT	CAAAAATAAA	CTAACACTGA	GATACAAACA
71551	GAAGTGGCAA	TGTTAAAGAC	TACTGTTCTG	TGGCTAGAAG	AACAAGTACA
71601	AAGCTTGCAG	TTGCAGTAGC	AATTGCGTTG	TCATTTTAAC	CATACTCATA
71651	TTTGTGTAAC	CAATTAGGAA	TATAATCAAA	GTGAATATCC	ATGGAACCTT
71701	GTAAAGGCCC	ATTTACAGGG	AGCTGTTACA	TCCAATGTTA	CTTTTGATAT
71751	TAATGATTTA	CAAAGTAAAA	TTCTAACAGC	ACCTCAATAT	CTTTTTCATA
71801	ATTATTGGAA	TAATGTTACT	ATGTTTCTGT	TTTTTGTTC	TAGTCTGTAA
71851	AATCAACTGG	AACACCAACC	AGCAATTGAG	AGCTGAACAG	CCTGCAATTA
71901	CCTTTATTCA	ATTAAATCAA	AAGCAGAAAG	GGGGAGATGT	TGGAGGCTGA
71951	AAGAATGAGG	GTCATGACCA	ACTCAGTATA	CCACTGGAGG	CTATGTGAGC
72001	AAACAGCAAA	CTGTTCTCAT	GAATACAGGA	TATTGGCAAG	CTGACAGCTG
72051	CATCTGCCAC	CAGAAGGAAT	GCTGAGGACA	GTCATGCATC	AGGCACAGTG
72101	TTCTTGTAG	TTATCTATAG	GAACATCTGG	ACCCTGTTGT	ATAAAGAAAG
72151	CAATTATTTG	AGCCTGTGAT	AAATCAAGCA	GCTGACTAAA	ACTGTTACCT
72201	CTTCCTCCCT	GTTGATTCTA	CCTAATACAT	GTGAAGGGCT	GTATAAGCTC
72251	AGGGCCCTTG	TTCCCTAGAA	GCAAGGAGCC	CCCTGACCCC	TTCTTTACAA
72301	CAAATCTTTT	TGTTTTTGTC	TTCATTTCTG	CATTATCCTT	CCTTCGTTCA
72351	GTCCCGAACC	GACAGCCACA	TGATCTGGCA	ATCCCATTTC	TGGATATCTA
72401	TATAAATGTT	CAAAGCAGGA	CCTGAAAGAA	ACATTTTACA	CCCCTGTTTA

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72451 TAAGAGATTT ATTCTAAAAA TCCAAAAGGT AGAAGCTACT TGAATGTCCC
72501 TTGACAGATA AATAAATAA AATAAATAT GATATATACA TATAATATGA
72551 TTTAAAAAGA AAATCTTGGG CTGGGTGTGG TGGCTCATGC CTGTAATTCT
72601 AGCACTTTGG GAGGCCGAGG TGGGCAGATC ACGAGGTCAG GAGATTGAGA
72651 CCATCCTGGC TAACACGGTG AAACCCCATC TCTACTAAAA ATACAAAAAA
72701 TTAGCCAGGC ATGGTGGCAG GTGCCTGTGG TCCCAGCTAC TCAGGAGGCT
72751 GAGGCAGGAG AATGATGTGA ACCCAGGAGG TGGAGCTTGC AGTAACCGGA
72801 GATTGCACAA CTGCACTCCA GCCTGGGCGA CAGAGTGAGA CTGTCTCAA
72851 AAAAAATAA TAAAAATAA AAATAAATAA ATCACACACT GCAATGACAG
72901 TAAACCTTTA GGACATAATG TTAAGTGAAA TGTGCCAGGA AACAAAGTGA
72951 CAGTGAGTGT ATGATTCCTC TTATGATATA TCTTAAGTAG TCCAACCTAC
73001 AGAAACAGAA AGTAGAATGT CAAAGGCTCA GGAGAGGGTA AAATGGTCGG
73051 TTGACGTTTA TGGCTATTGA GTTTTAGTTT TGCAATGGAA AAGCTCTAGA
73101 AGCCTGTTGC ATAACAATGT GGATATATGT AACACTACTA AATTATGCAA
73151 TTACAAAGGT ATAGACTGGT AAATTTTGTG GTGCTTTATT ACAATTAAAA
73201 TATTGTAAAG TGATACATAA AAGAGATACA GAGTTATAAA CTTTTCAGAA
73251 AATTACCTTC AAATTATAAG CGTGTTTTTC TCACACAAAG ATAATATAGA
73301 TTCATCAAAA AATACATGGG CAAATTAAGA CTATTTACAT GACTACTCTC
73351 CTGAACAAGT TAAAACAAAC TTTTGACATC AGCCAAGAAG AGAAATATGC
73401 AAGATAAGAA TAAATGGAGT ATATTTATAG AGGCAAACAA ACACATGATT
73451 TTATTGGTGG TAGATATGAC TGATTCATAT TTTAATTAAA CCCCACATCG
73501 ACTCGATGTG TACATAGAGT TGCAGATTTA CATCCAAAT CATAATATGT
73551 AGGTAACACC AAATTCACAA AACACAAATG TCAAAGAAGC TACCCCAAAA
73601 AAGAAGCACA GTAATATGAA ATTTCAAAAC AAGAATGAGA GAAACATTAA
73651 CAACAACAAC AACACAACAA ACACTTCTAT ATAAAAATA GATGTACAAT
73701 TAAGAAAGAA TCCGCTTAGA TAATTACAAT TTCCCGCTGT GACCTTGCAC
73751 TGGTGGTGAG CACAGATTTT GAATCATGAC TATGTTAGGG AGACGCCCAA
73801 GGAGACAGAC AGTGCCACCT CCAGAGAAGC CATTGCTTCT CCTCCTGCCG
73851 CTGCTGCTGC TGCCCCCACC GTCCGCTGCG CCTGCAGCCC CCACTGAGCG
73901 TCGGACTCCT TCCTGGAGTA GGGAGGTCTT GTTCCTTCTG GAGCGACAGA
73951 CACCCTTTCT CCTGGCCTTC TCGCTTACTA GCCCGGCAGG TGCTGGACAG
74001 GAGATCTGAG CTGGTCTGTC GTCTCTGAGG AGCTAGGAGC CCGGCTGGGA
74051 GAACAAGGAG ACGAACTGTG GGGAGAAGGG GCGACAGGAA CGCCAGGCTC
74101 ATGGGACCGC TGGCAGCGCG CTGGGTATGG CTGGCGGCTG AATGGTCAGA
74151 GATACGAGAG GTGGCCACTG TCCCCACCTT TGGCCCCCTA GCCGGCATTC
74201 GTACATTCTG TGCTCAACAA ACGGAAGCGG CAGCTGGAGC TGCTGCTCCG
74251 GGAGGTGGAG TGGCCTGGCA GAGGGCACAT GGCTGCCACC TGCTGCAAGG
74301 TGAGCTGGTC TGCAGCCTGG GCCCACAAAA GGCCGCTCTT GTGCAGGACA
74351 CACCGCTGCC CTTGACCCTC TTGCTCCCCC GCCTGCTGTG CAAAATGCTC
74401 AGGTCCCTGA TCTCGGGCTT TCCTGGCAAG TGCACTGTGG TGGGGAGGCA
74451 GCAGGGAGGA GGGCTTTTCC AGGAGCCCTG AACAGAGGAT CTTGGCATAA
74501 AGAGGAGAGA GAGGTGGCTG ACTGGTTCCA CTTGTAGGTA GGGGGGCAAC
74551 AAACCCCATG GGACCCTGTT TTTTCAGGGA GATTTCAGTT CACTTCTTAT
74601 CTTTTCTCCA CCCACTTGAG CCTCTGAGAA TAGAGGAGAC GAGGCTGTTT
74651 TAAATTGGCC TAACCATAAT GGTCTGGACC CTTGCCCCAG GGCAGACCTA
74701 ATTTTGGGGC TCTTTGCAGC ATGGAGGCTC ACGCCTGTCC ACCCCAGGTG
74751 TCTTCAATAT AGGGTCTAGT TAGGCCTGGC TGGCAGTGAT GCTGAGACGC
74801 AGCACGACCT GGCCAGATCT TCGCCTGTTA CAGGACATTA TAGCCTTCAG
74851 TGCCCTGTGC CATTTATCTC GCCTCCAGAA GCCCCTGTGA GCCTCAGTGT
74901 TGCCGGTGCC CAGGCCCTGG CTGCCTCTCT ATTAGGCTCC CATCTTATGC
74951 CTCTAAATG CACCGGGGTC TCACTCTGCC TTTCTCCCTT TCCCAGAACA
75001 GGCCCTTCA ACTCCAACAG AACATGCCTG GACCATGTGC ATCCCTCTTC
75051 AGTGTTAAAA CAAAGAAAAT TTATTTTTTT TCCACTGAAC ATGTAAGTGA
75101 TTTAACATAT AAGGAGGTCA GCTTTATGCA TAGATCTATG CATGTAAATA
75151 TATACAAAAA TTCTAACGCT GTGGGAAAAT TAACATCCTT ACACTTTGTT
75201 CAGTTATTTT ATAGTTTTCT CTCTCTCACT CAATTGCTTT TTTTTTTTTT
75251 TTTTTTGAGA CAGAGTCTTG CACTGTTGCC CAGGCTAGAG TACAGTGGCA
75301 AAATCTCAGC AACTGCAGC CTTTGCCCTC TGGATTGAGG AGATTCTCAT
75351 GCTTCAGCCA CCTGAGTAGC TGAATTACA GGCATGGGTC ACCATGCCCA
75401 GCTGTTTCAT GTGTTTTTTT TTAGTCGAGA CCGGGTTTTG CCATATTGCC
75451 CAGGCTGGTC TCGAACTCCT GGTCTCAACT GATCTACCCT CCTTGGCCTT
75501 GCAAAATGCT GGGATTACTG GCATGAGCCA CCATGCCAG CCTACCTGTC
75551 ACTATCTCTA TGTTTATTG TTCAACAGGA AAATTCTCAG TGAAGACTCC

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75601	TCAGTATGAA	GGAGATAAGC	CTGCACAATC	AGTCACTGAT	AGATGCTTAG
75651	TGGAAAAACT	TCCAATTCCT	ATTTACAGCT	CTCAGAGCTA	GGATTAAAAA
75701	CTCCTGGTCA	TAAACTCATG	TGATGAGAAG	TTATAGCACG	CCCTCATTTT
75751	CTACATATCC	ACTTGCATTT	ATGGTTGGCT	TTTGAAGTTG	CTAGAAGGGA
75801	AAGAAGTGCA	AATGTGTCCT	CCTTAGAGCT	ACTCTCCTCC	CCTTGGTGGG
75851	TTTCCAGTTT	GTGCATTGTC	CAGATGGCCC	AGGAGCTGAC	GATCAAAGGG
75901	AAGAAGTCAT	GTTTGTCTAT	AGAATGCTTT	GCTGCATCAG	GATTCAGTGA
75951	AGCTGTTTAC	CGCCTGGAGC	CCATGCAGCC	TCAAGAGGCA	GGATGGAGCT
76001	CAGAAACCAT	CACTGAGGTT	AGAAAGTGAG	CACCAAAGTT	GAGGGAAGCC
76051	CACAGGAGTG	AGCCGAAGTG	CTCCCTTTGG	ATTTCCAAGT	GGTTGCTGCT
76101	GCTTCTTCCA	TCAGCCTTGC	TTCTGACCAC	AATGTGTTCC	TGGTGCCTTC
76151	TTCTTGGCAT	TTTGCTGTTT	GTGTCCAAGG	AAAATAGTCC	TGCATGGCAG
76201	TGGTGAGAAG	GATGGCTGCC	TGCTGAAGCT	GATTTGCTGG	TAAGCTTTGC
76251	AGCCTGTAA	GCAGAGCCTG	AAATTCTTTC	TCACTGAGTG	GTGATTCAAA
76301	CCTTGGAGGG	TCCCTCCCCTT	GTGGATCGGC	ATTCAGAAAA	GATTGTGCCT
76351	TTTCTGAAA	CTCTGGGGAT	TATAGGAGAT	CATGCAGATG	GCTGGTGTGG
76401	TTGCTCCAGC	AGGTGGATGT	CTCCTTCGTG	GCTTGTGTCT	GTTTCTGTCA
76451	CAGGGGAGAC	TCAGTGTGCA	TGGGCTGCTA	AGGTGCTCCT	GCTTCAGGTT
76501	GAATCATGAC	ATCCTAGGAC	CCCTTGCCCC	GGCTCCACCA	CTGCTGGGAT
76551	TTGGCCTGTT	GACCCAACT	CTAAAATTGT	GGCTAAGAAT	GACCAGGCTG
76601	AGGCTGTCTT	TTAAGGCAGA	ACTTCCAGGT	TAGTGTCTCA	TTTTTCTTAT
76651	CCTGAAATTT	TCCTTTTCGAC	AGAGGCCAGA	AGCAAGTCTG	TGTATGGGAG
76701	AGCCTCCCTC	CTAGAGCTGG	TACCATTGAC	ACATGACTCC	TGAGTGCCAG
76751	AAGAGGTTGA	GAGAACTCTC	CCATCTGCAC	AGCCTGTCTC	ATGCAGAAATG
76801	CAGATGGATC	CAAAAAATCA	CAGGATGTGG	GAGGTGAAGG	AAGAGCTTGT
76851	AAAAATGAAA	AGTGGCTGGT	GAAAGAGTAG	GAGGCATGAA	GAGGATGAGA
76901	CCTGCCTGGG	GCAGTGCACA	TGTTTTGTTC	CAGCCAAACA	ATCAGATGAG
76951	GTCTTGGTCT	TGGACCTGGT	GCCAGGGAAT	TCATAAGCCC	CCTTTTGCTG
77001	TGGCCTGGGA	GCTGAGGTCT	TTGGTTCTGA	AACCAAATGT	AAATTTTGA
77051	CTCTGGAATA	CCTGTCTGTT	TAACCAAGTTT	CTCTCTACTG	GTGATCGCAG
77101	GAAATGAATT	ATCCTGTAAA	ATTTTGTGGA	TTCTTCTCAA	AGGCTTCAAT
77151	GAGTACACTG	ATTTGTGGTT	CAGTGATGGA	TGTCCTTTTC	CTCCTGCCTT
77201	CTTATTTGAC	TTACACCATC	AATATTAAT	ATGGCAGTTA	TGGTAATATC
77251	ATTCCTTTACA	ACAGAGGAAA	CTTCAAGTCA	TTCAATTGATG	ATATCAAAGC
77301	CTCATTCTCC	TACATTAAAC	ATTCTCCTAC	ATTTAGCTTC	TTGAATCTTC
77351	TATGTCCACT	GTCTAGAAAA	CCTAAACACA	TGAAGTACCA	CAAACCTAGAA
77401	ATAAATACCT	CAATAGGCAC	CAATCATAAA	AGTAAATCCA	AGAAGGAACA
77451	GAATATATGA	ATACATATAT	AACAAGTAAA	GGGATTCAAT	TAATTAATAA
77501	TCATCACACA	CAAAAAAGCC	CAGAGTCATG	TGGCTTAACT	GATAAATTCT
77551	ACTAAACATT	TAGTGAAGAA	TTAATGCCAA	CTCTTCACAA	GGCCTTCCAG
77601	AAAATAGAAG	ACAGTTATTG	GGAACACTTC	CCAATTTGTT	CTATCAGGCC
77651	AGTATTACCC	TGATACTAAA	GCCAGACAAA	AGCATCACAA	GTAATATGTA
77701	ACATAGATGA	ATTTCCCTGA	TAAATACACA	AACAGAAAAA	CTCAAAAAAG
77751	AGTGAAATGA	ATCAAGAATA	AATCAAAATG	ACTGTACACC	ATGACCAAAT
77801	GGAATTATTT	CACAAATGCA	ATATTGATCT	ATCCAATAAT	CAATCAATGC
77851	ATTACACAAA	GTAATAGGAT	AAAGGAAATT	AACAGAAAGG	TCCTTTCAAC
77901	AGACACAGGG	AGCATTTAAC	CAATCCAATA	TTCATTACAG	ATCTCCCTGG
77951	AAAAGAGGAG	TACAAGAAAC	TTCCTAGATC	TGCTAAAAGG	CGTCAATGTA
78001	AAACTTACAG	CTAACCCCAT	AATAATAAAA	TACTGGTTGT	TGTGTCTTGA
78051	CATTTGAGAA	CAAGACAAAA	ATGTTAACAT	CCAAATAAAT	TACATAAGAA
78101	AAATAAACAA	AATCATCAAT	GTGGGAAAAA	AAGAGGTTAG	AACTCTCTAT
78151	CATTGCAGAG	GACATAATGT	GAATATAAAA	GTTTATAAGA	AATTCATTAA
78201	AACTCACTAC	AACCAATAAG	TGAGTTCAGC	AACATCACAA	GATACAAAAC
78251	CAATATACAA	AGTTCAATCG	TACTTTTATG	TACTAACAA	GATCAACCTG
78301	AAAATAAAAT	TAAGAAAACA	ATTCCATTG	TGTATGTATG	AAAAGGAAAA
78351	AAAATATTTA	GGAGTAGATT	TAATCAATTG	CAATTTTACA	GTAAAAAGAA
78401	AAACTGTAA	ATAACTTTTA	AAAAGTAAA	AAAATAGGCA	TCAAGGTTTA
78451	TTTAGTTAAT	ATTATTCCAT	TATTCAAGTG	ATCCATTTAA	ACTCCATACA
78501	ATAAATAAAA	GTATATTTTA	GCATTATTTT	TAGTGTAAAT	AATACAGGTT
78551	GTAGAAAAAC	TCATAAATAT	AAAAGGAACT	AATACTACAT	GTGCAGAGTA
78601	GCCCATTTCTA	GTTTTTCTAT	TTTACATCTA	CTGTAAATCA	AACAGATTTT
78651	CTTCCATATT	TTATAGTGGA	TCTTAATATA	AAATCCAAAT	TGTTAAATAT
78701	GTGAGATTGA	TTATAAGCTT	GCCAAGGAGG	TTTTTACTCA	GTGTGGGAAT

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78751	TTGGAGAGCA	TAAAGCTGCA	AAGACAGAAG	CAAATGTTTT	TGAATGAATT
78801	ATGAGGGACA	ATACTCACAG	GAGTGATTCC	CACTTTTATC	AGTTGACTCA
78851	TGTGATCTTA	CTTTAGGAGA	AACTGACTCT	CATTTTAGAC	ATTGGTTCAT
78901	CACAGATGCT	AAATGAACCA	GCACCAAGTT	TATATCCAGG	AGAACTGCTC
78951	ACTGTAGAGG	ATTTTGTCTC	CTAGCTGATG	ACATGTCTTG	TCTTTCATAG
79001	GCTACTCCAA	AACTTTTATA	ATGATGGTAG	AGTTCTGTAA	AGTGGAGCCT
79051	CAGGCCTGCT	ATCCCCATGC	TCTGGCCAG	CAGCAGCATC	TCCCCTGAGC
79101	ATGGTGACAT	AGGGCATGCC	ATTGACACCC	AATTTGCTGG	TGTTCACCTC
79151	CACATACTAA	GTTGCTAGAG	AATTTGCAGT	GGATTTCCAT	TTTGCTGCAT
79201	CTGGCTGTCC	AGAAGCCCTG	CAAGTAGAAT	GGGATGGTCA	GGAGAAAACA
79251	TTGAAAGAAT	AGATGGGAGT	TCAGAGGCTG	CCCACCCTCC	TGCCCTCTGC
79301	CCACGGGCCA	CAGCCCTCAC	CCAGCTGTCC	AGTGTGTATG	TCTGCTAAAG
79351	GCTGCTGCAC	TTGTTCTCCA	TCACAGAGGT	GGGGTGACAG	CAGTCTGTGG
79401	GCACCACACT	CCATGATCAG	CCTCTACTGT	TGGTGCCACA	GCTCCAGGTA
79451	GAAGGGCAGG	TGAGCCAAAG	ACAGGTCCCA	CCTTCCACAT	CCAGCCCACA
79501	TTCCCACCAA	CTTCCAGGCC	CACCTCCATA	TGCTGATGTG	ATGCTCTCCT
79551	TAGAGCTCTT	GTGGTTCTTC	AGCCAGGAGA	TGGAGAGAGT	GGGGTTTCAA
79601	GAGTAAGGCA	GTGAAAGTTG	GTTTGGGTGG	CCACCATGGT	TGGTGGTTTC
79651	CTGTCCATCC	ACTCGGTCCA	AGTCCAGTAA	GGGGCCTCTG	CTGGTGGAAG
79701	CACACATGAA	GGCCATAGCT	GGGGTGAGGA	GCAGAGACTT	ATCTCACCAG
79751	ACCCCCAATT	CAAGGTTGCC	GCTGCCCCACC	CACACCCTCT	CTTTTCCCTC
79801	CTGTGTAGGG	AGATTGTTGG	CCTTTCAAAC	CCCTCTTCCT	GGGCTGAATA
79851	AGGATTCCAG	GAGCTTCAAC	ATAATGTCCC	CACCCAGTCA	TGCTCAGAGC
79901	TGGGCCATGT	GTCCCCTCCC	ATTCCCTTCA	CTTCCCACAA	GTGGCTGCTC
79951	CTGCTGAGAG	GTTGGGGTGC	TTCATCCTGG	CCTAAAAACC	TCAAAGAATA
80001	ATGGAGTCTC	CAAAGGAGCC	CCCACCCACC	CAGGGAGGCT	GACAGGGAGG
80051	GTCCACCAGG	AAGGGAGCCC	AGCAGGTAGC	CCAGCTAAGT	GAATGAGCCA
80101	GGGTAGGCAT	TGGGAGCAGT	TTACCAGGAG	AAGAAACTCA	GCCCCTTGCA
80151	GAGCGGGGAG	CCTCAGAAGC	AGCAGAGAAG	CCTTGCCCCA	CAAGACTCTG
80201	AGTCCCTAAG	CCACCCCTTG	TAGAGCTCCA	GGGCACTGGT	GAGGATGGCC
80251	TCCTGGAGGC	CTCAGCTCTT	TTTTGTGCTA	ATGTCCAGGG	CTGTCACCAT
80301	TCCGCCCCCG	CCCCCCTCAC	AGCTGAACCTA	TTTTTCTTCT	TTCTGGGGCT
80351	GGGGTGGGGC	TGCCTTCCTG	CCTGGATTCA	TGGGTAGGCT	GGATTGCCTT
80401	ACCCCCAGGA	GAGAGGCCAC	AGGGGCCCAG	AAAAGAGGAA	GGAGGCAGCC
80451	CCTTCCCCAC	AGTGACCTCC	TCGCAATTCA	CATGCAGCAA	CAGGCCACC
80501	TCTCAGAGTA	AGATGCTGAG	GCACAGGTAG	GAGCTGTGTA	GAGAGACACT
80551	GGGAAGAGGC	ACCTCTCACA	GCTCTGAGCT	GACCTCCAGC	CCTCCAGGGA
80601	TGGGGGAAGG	TAGACCCATT	GGTGATGAAG	ACAGCTCAGT	GAGCTGTGGC
80651	AGAGGAAGTT	CCCAGGACTG	GGAGACGACA	GTGACTCAAC	GCTGCTCATT
80701	TCTAGACTGT	GCTTTCTGAA	AGTGGCCCTT	CAGTTACCCC	CACAGCTTGA
80751	GGCCACACAA	GCCTGGGATG	GCCAGTTAGG	CAGACGCAAG	CAGGGATTCA
80801	GGGGGAGTGC	ACTAGGGTGT	GTGGGCAGGG	GCAGAGGCCA	TTGAGGCAGG
80851	TGAGGAGAAA	TTTTTCATCCT	CTTCTGTGTC	TGCCCTCTC	CTGGGGTCTA
80901	ATTTCTCTTA	TTCCGTCTGC	CTCTGGCTCC	CTGGCTGGCT	CCTCTTCACT
80951	CTCTTGCTTG	CTCACCCAG	AGGTCCCAGG	GGCTCAGCCC	ACCACAAATG
81001	GTCCCCAAGT	TGTAGCTGAC	CCTTCCATGT	CCATCCCATG	AGGACCCTCA
81051	TCTGCCTGAG	TATATCTCTG	GGCTCCTCTG	AAACCAGAAG	TCCCACCTCA
81101	CTGACTGCTC	CATGGCTAGG	CAGCATCCAC	CTGCCACTGT	TCCAGGCCAG
81151	AATGACTGGG	CATTGTCCCC	CTGCCTGCTC	CCTCACACCT	ACAGCTCATG
81201	CCCCAAAAT	GCTGTTGGCA	TCCTTCATAC	AACCTCACA	GCCACCCTGC
81251	CCCTTGCTGG	GCTGTAGGTT	TGGTCTCCTG	GTGCCTTAAC	CCCTTTGTCC
81301	ATCTGCCCCT	GGGCAGCCAC	CTGAGCCCT	GAGCACTGCT	GTGCTCACAT
81351	GTGCAGTAGC	CCCTCACACC	AGAGCCAGCA	TCGAAGTCTC	CACAGGCCAA
81401	TTCTGGCCTC	ATCACTGCTC	CTGGAACCCC	AGGGCCCTGT	GCCCCAATCT
81451	CCCCATCTGC	AGCATGGGTG	TCTCTTCCCTA	CCCCAAGCCT	GCCCCCAGA
81501	GCTCAAGACA	TCCAGAGCCA	TCTAATACAT	ATGTAATACA	TACAAATTAC
81551	ATAACAATTT	GTAATATGTT	GTACTACATA	CACATTTTCA	TATGAATTCA
81601	TCATAATACG	TACAAATTAT	GATGTCATAA	TATATTGTGA	TGTGACAATA
81651	CACATGAATT	ATCATGTGAT	AATACATTGT	GATGTCATAA	CACATACTAA
81701	TTATGATGTC	ATGATATATT	GTGATGTTAT	AATGCATATG	AATTATGGTG
81751	TCACAATACA	TATGAATTAT	GATGTCATGA	TACATTGTGA	CGTAATAAGA
81801	ATTGTGACAT	CATAATATAT	CATGATGTCA	TATGCATGCA	ACTTATGATG
81851	TCATGATATA	CTGCAATGCC	TTAATACAAA	CCAATTATGA	TACAGTAATA

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81901	TGTTGTGATG	TCATAATATC	ATATTTATTT	ATCATATTTA	TCATATAACA
81951	TTTTGTGAGA	TATTTTTATA	AGAAAATTGA	GTGAAATTTT	GTAACATTAA
82001	CATATAAAGA	AGCTTACAAT	CATGATGAAA	GATGAAAGAG	GAGCAGGCAT
82051	CTCACGTGGT	AGGAGTGGGA	ACAGGAAAGA	TGGGGGAGAG	ATACGCCTCA
82101	CTTTTAAACC	ACCAGATCTT	GTGTGTACTC	ACTGTGACAA	TGACAGCACA
82151	GAGCCATGAG	AAATCCATCT	CTATAATTCA	TCCACCTCTC	ACCAGGCCCC
82201	ACCTGTAACA	TCAGGGATTA	AAATTCAATA	TGAGATTTGG	AGGGGAAATC
82251	TAAACTATAT	CATATGACGA	TTAGAAAAAC	AGATGAGGTC	CTTCACGTCT
82301	CTTTGAAGCA	ATTGTGAATG	GGAGTTCACT	CATGATTTGG	CTCTCTGTCT
82351	GTTATTGGTG	CATAAGAATG	CTTGTGATTT	TTGTACATTG	ATTTTGTATC
82401	CTGAGACTTT	GCTGAAGTTG	CTTATCAGCT	TAAGGAGATT	TTGGGCTGAG
82451	ACAGTGGGGT	TTTCTAGATA	TACAATCATG	TCATCTGCAA	ACAGGGACAA
82501	TTTTACTTCC	TCTTTTCCTA	ATTGAATACC	CTTTATTTCC	TTCTCTGCC
82551	TAATTGCCCT	GGCAGAAGCT	TCCAACACTA	GGTTGAATAG	GAGTGGTGAG
82601	AGAGGGCATC	CCTGTCTTGT	GCCCGTTTTT	AAAGGGAATG	CTTCCAGTTT
82651	TTGCCCATTC	AGTATGATAT	TGGCTGTGGG	TTTGTCTAG	ATAGCTCTTA
82701	TTATTTTGAG	ATACGTCCCA	TCAATACCTA	ATTTATTGAG	AGTTTTTAGC
82751	ATGAAGGGTT	GTTGAATTTT	GTCAAAGGCC	TTTTCTGCAT	CTATTGAGAT
82801	AATGATGTGG	TTTTTGTCTT	TGGTTCGTGT	TATATGCTGG	ATTACATTTA
82851	TTGATTTGCG	TATATTGAAC	CAGCCTTGCA	TCCCAGGGAT	GAAGCCCACT
82901	TGATCATGGT	GGATAAGCTT	CTTGATGTGC	TGCTGGATTC	GGTTTGCCAG
82951	TATTTTATTG	AGGATTTTTG	CATNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
83001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
83051	NNNNNNNNNN	NNNNNNNNNN	NNNTTTTAGG	GCAGGCCTGG	TGGTGACAAA
83101	ATCTCTCAGA	ATTTGCTTGT	CTGTAAAGTA	TTTTATTTCT	CCTTCACTTA
83151	TGAAGCTTAG	TTTGGCTGGA	TATGAAATTC	TGGGTTGAAA	ATTCTTTTCT
83201	TTAATAATGT	TGAATATTGG	CCCCACTCT	CTCTGGCTT	GTAGAGTTTC
83251	TGCCAAGAGA	TCCGCTGTTA	GTGTGATGGG	CTTCCCTTTG	TGGGTAACCC
83301	GACCTTTCTC	TCTGGCTGCC	CTTAACATTT	TTTCCCTTCAT	TTCAACTTTG
83351	GTGAATCTGA	CAATTATGTG	TCTTGAGATT	GCTCTTCTCG	AGGAGTATCT
83401	TTGTGGCGTT	CTCTGTATTT	CCTGAATCTG	AATGTTGGCC	TGCCTTGCTA
83451	GATTGGGGAA	GTTCTCCTGG	ATAATATCCT	GCAGAGTGTT	TTCCAACCTG
83501	GTTCCATTCT	CCCCGTCACT	TTCAGGTACA	CCAATCAGAA	GTAGATTTGG
83551	TCTTTTTCACA	TAGTCCCAT	TTTCTTGGAG	GCTTTGTTTG	TTTCTTTTTA
83601	TTCTTTTTTTC	TCTAACTTC	CCTTCTCGCT	TCATTTCAAT	CATTTGATCT
83651	TCCATCACTG	ATGCCCTTTC	TTCCAGTTGG	ATCGTATCAG	CTCCTGAGGC
83701	TTGTGCTTTC	TTACAGTAGT	TCTCGAGCCT	TGGCTTTCAG	CTCCATCAGC
83751	TCCTTTAAGC	ACTTCTCTGT	AGTGGTTATT	CTAGTTATAC	ATTCCTCTAA
83801	GTTTTTTTCA	AAGTTTTCAA	CTTCTTTGTC	TTTGGTTTGA	ATTCCTCTCT
83851	GTAGCTCGGA	GTAAGTAGTT	TGATCATCTG	AAGCCTTCTT	CTCTCAACTC
83901	ATGTGGAGAA	ATAGGAACAC	TTTTACACTG	TTGGTGGGAC	TGTAAACTAG
83951	TTCAACCATT	GTGGAAGTCA	GTGTGGCGAT	TCCTCAGGGA	TCTAGAACTA
84001	GAAATACCAT	TTGACCCAGC	CATCCCATTA	CTGGGTATAT	ACCCAAAGGA
84051	CTATAAATCA	TGCTGCTATA	AAGACACATG	CACACGTATG	TTTATTGCGG
84101	CATTATTAC	AATAGCAAAG	ACTTGGAACC	AACCCAAATG	TCCAACAATG
84151	ATAGACTGGA	TTAAGAAAAA	GTGGCACATA	TACACCATGG	AATACTATGC
84201	AGCCATAAAA	AATGATGAGT	TCATGTCCTT	TGTAGGGACA	TGGATGAAAT
84251	TGGAAATCAT	CATTCTCAGT	AAACTATCGC	AAGAACAAAA	AACCAAACAC
84301	CGCATGTTCT	CACTCATAGG	TGGGAATTGA	ACAATGAGAA	CACATGGACA
84351	CAGGAAGGGG	AACATCACAC	TCTGGGGACT	GTTGTGGGGT	GGGGGGAGGA
84401	GGGAGGGATA	GCATTGGGAG	ATATACCTAA	TGCTAAATGA	TGAGTTAATG
84451	GGTGACGAC	ACCAGCATGG	CACATGTATA	CATATGTAAC	TAACCTGCAC
84501	ATTGTGCACA	TGTACCCTAA	AACTTAAAGT	ATAATAATAA	TAAAAAAAAG
84551	AAAGAAAAAC	AGATGAGGCT	GGGTGCAGTG	GCTCACGCCT	GTAAACTCAG
84601	CACCTTAGTA	ATCCGAGGTG	GGCAGATCAC	AAGGTCAGGA	GATTGAAGCC
84651	ATCCAGTCTA	ACACGGTGAA	ACCACCCCA	TCTCTACTAA	AAATACAAAA
84701	AAATTAACATG	GGTGTGGTGG	CACTCAGCAG	TAGTCCCAGC	TACTTGGGAG
84751	GCTGAGGCAG	GAGAATCGCT	TAAACCCTAG	AGACAGGTAT	TGCAGTGAGC
84801	TTAGGTCATA	CCACTGCAC	CCAGCCTGGG	CAAACAGAGT	GAGAATCCAT
84851	CTCAAAAAAA	AAAAAAAACA	AAAAAAGAAA	AGAAAAACAG	
84901	ATGAAATAGT	AATGGTTTCT	ACAGATACTT	TCATTACAAA	GCATATGGAT
84951	AAATGATTTA	ATTCAACATT	CTGTGGTCAG	AAGAGAGAAG	GGAGGTGTAA
85001	AGGGGACTTT	GACTGCATTT	GTTATACTTC	CCTTATGCTG	TTGTTATGAG

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85051 TTTTGATGTC ACCACCTGAA GGGGTATTCA TGGACGGAAG AATTATTGCT
85101 ATTGTGTGA TTATTCCTTT TTCTTTTGTA TTAGTAAAAT AAATCTTTTA
85151 GCTTCTCATA TAATTTTCTT TAAAAGCCCT AAGAGTTTCG GTTAAATTCT
85201 TCGTTATTGT GTGTTATAAA AATTGACAGG GAAATGGCTA AAATAGGTTA
85251 AAATTACACA AACTCTAGGA GTCCAGTTTC TGTTAGACAG GCTTAGGAGA
85301 GACAGAACTG GAAACACTCC ACCATCATAG ACATCAGACA CATGGGGCTC
85351 ACTTTCTGTC CCAGCCCTGC CCAGATCCAC CCTCTTCTAA GGCCTTATCC
85401 AGGCCTGGCC TCACCCTAGA ATCTCCTCTC ACAGAAGGAG ATCAAAATTA
85451 AAGGAGATCA AAAATTTGAG TGGTGGCTCC TCCTGCCTCT CTTAGCTGA
85501 TGCCCACAAT TTCCTGAAAA TAAAAAGCAG ATAAATGGGA GCAAATGATT
85551 ATCTATTGT GGGTCACAAT TTCTTTTTC TGAAGCCAG TGCTTGTA
85601 GACATCCAC CTAGCAAAC GTTTTTCTGC CGATCCGTA GATGCTCTAC
85651 AAAGCACAAG AAAGTCAATA TAAATACCAA AAATCCCTCT GAACAGTTCA
85701 CCCTTTCTGT ATCCCTTCCA TCTGTCTATA TAGATTTTAT TCTACACATT
85751 TTCTTTTAA GGTAAGTAAT TTAAAAATG AAAGAAAAAT AGAAATGCTG
85801 GGCCCTTCAT TTAAAGCCTA GGAATTACAG AACACTTAGC AGCCAACACTAC
85851 CAGGGTTGAG GATTCACCTA CATCAGGTGA TGTTTGCAGC ACAGTGCTGT
85901 GTAACAGACT TCTGAACACA TAGTACACAC TCAGTAAACA TTGTATTAAAC
85951 TCATGGATAC ATGTTTTTCA AATGCAGACT TACTCAACCA TTGATGCCTT
86001 CTCTAGGCTC TATAACCTTT AAAGAGCCAG CAGAGAATAA CATGTTTGTA
86051 TATAGTGATT GGTGGTTTCC ACTTTGGGCC AAAAGGGTTT GTGTTGTGGT
86101 AAGAGTGTG GGTGTCAGGA ACTCTCTGTG CTGTTCTAC TTTCTCTGAG
86151 TGCTACTACA GTGGATATAG TGGGAGAATC AACAGTCTCC CCTTAAGGGG
86201 AGACTTTAAG AAGCCAATTC ATGGACCCCT TCCAAACTTG CAGAATCACA
86251 TTACTAAGAC AGAGGCTGG AATCAGAAAT GATTTATATG TACATTGAAA
86301 CTTGAGAGGC AATTCTTTGC TAAGTGGCTC TCAGCCTAGG TGTCCAATCA
86351 TAATCACATG ACCACTTTAA AGAAATACCA TCACCTGTGC TCTCCCACA
86401 GGTTCGTCT GTTGAGCTTG GTGGGCTCAT ACATATAGTT TTAATTAGGA
86451 AGTCAAATTG TCCCTCTTTG TTGATTACAT AATATTATAT CTAGAAAAAT
86501 CTAAAGACCA CCAAAAACTT TTAGATTGA TAAATAAATT TAATAATGTT
86551 TCAGGATACA AAAATCAATG TAGAAAAAGT AGTAGCATTT TCATACACTA
86601 ATAATGATCA AGCTGAGAAC CAAATTAATA GGTGAGTTT TTTTACAATA
86651 GCTACAAAA AGTAAACAC ATAGAAATAT AATTACTTAA GTAGGTGAAA
86701 GATCTCTACA AGGAAAAC TAAGAACTCTG ATGAAATAA TTGTATATGA
86751 CACAAACAAA TGAGAAAAAC ATCACATGTT CATTGATTGG AAGAAGTATT
86801 ATCATTAATA TGACCATACT GCCCCAACAG TCTACATATT AAGTGTAATT
86851 CCTACAAAA TTCTAATGTT AGTTTTTATA GAATTAGAAA AAAATTATAT
86901 TTATATGGAA CCATAGAAAA GCCTCAATAG CCAAAGCAAA TTTGATCAAA
86951 GACAACGAAG TTGGACATAT TACATTACGT GACTTAAAT TATTCTAGAA
87001 GGCTTTAATA ACCAAAACAG CATGGTAATG ATGTAACAG ATGCACAGAT
87051 CAATGGAGCA GTATAGAGAA CCTAGAAATA AAGCCATATA CCTACACACA
87101 ACTGATCTTT TCCAAAGTCA ACAAACAC ACACAGAAAA ATGACATTTT
87151 ATTCAACATA TTGTGCTGGA AAAATTACGT TACTATATGC AGAAGTATGA
87201 AATGGAACCC CTAACCTCTCA CCATATACAA AAATCAACTC AATATGGATT
87251 AAAAGGCTAA AATGTAAGAC CTGAAAAGAT AAAAATTCTA GAAGAAACCC
87301 TATGATAAAC TATTCTGGAC ATTGGCCTAG ACAAATAATT CATGACTAAG
87351 ATCTCAAAAG TAGATGCAAC AATAACAAAA ATAGACAAAT GGAACCTAAT
87401 TAAACTGAAA AAGCTCCTGA AAAGAAGCTT TTATTTAATA GGTGAGCAGA
87451 CAAGCTATGG AATACAAAAA AAATGTTTGC CAACTATGCA TGTGACAAAG
87501 AACTAATGTC TAGAATATAT AAAGAAATCA AACATCTCAA CAAGATAAAA
87551 ACAAGAAACT TCATTAAAAA GCAGGCACAT AACGGGAAAA GATATTTTTT
87601 AAAAGAAGAC AATGATGGCC AATAAGCATG TAAAAATGC TCAACATTGC
87651 CAATGATCAG AGAAATGCCA ATTAATAACG ACAGTGAAAT ACCATTTTAC
87701 ACCAATTCATA ATGGCTAATT ATTAATAAGC AGAAAAATGA TAGATATTGG
87751 TAAGGATACC GAGAAAAGAG AATACTTATA CATTGTTTGT GGGAAATGTAA
87801 CTTTCTACAG CCTCTATGGG AAACAGTATG GAGATTTCTC AAAAACTAA
87851 AAAATAGAAC TTCCATTTGA TCCAGCTATC CCACTACTGC GTATCTACCC
87901 AAAGGAAAAA AATTCACACT ATAAAGAAGA TACCCACACT CATATGTTTA
87951 TTGCAGGATT ATTCAACAATA GCAAAGATAT GGAGTCAATT TAAATTTATC
88001 TATCAATGAT TGAATAAACA AAATTTGCTA TACATTTATA CCATGGAAAA
88051 CTACTCAGAC ATAAAGAATA AAATTATGTC TTTTGCAGCA CCATGAATGG
88101 AACTGGAGGC CATTATTGTA GGTGAAATAA CTCAGAAACA GAAATCAAA
88151 TACTGCATTT TCTTACCTAT ATATGGAAGC TCAATAATGC ATACACTTGG

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88201	ATATAGAGAC	TGGAAAAATA	GACACTGGAG	ACTCAGAAAG	ATAGGAGGTT
88251	GGTAGAGGGG	TTAGAAATGA	GAAAAACACC	TAAGTGGGAC	ATGAGCACCG
88301	TTCAGGTGAT	TGTTACACCG	AAAGCACATA	CTTCATCACT	CTGCAATATG
88351	TCCCTGTCAT	GAAACTTCAT	TTGTACTAAC	ATATTAATAA	AGAGAAAAAA
88401	ACTGACTTTT	ATCAAGAGAG	CAGAATGAAT	AGACCTTCTA	CTTTTCATAA
88451	ATACTTAGGC	AGAAAAATAA	TTTAAATAAA	AATAAATAAA	AAATGTATAT
88501	TATATATATT	TTACATAATT	TATATATTGT	AAATATATAT	CAATATTTTT
88551	ATATATCAAT	ATTTGTATAT	ATAAAAATATA	TATCAATATT	TTATATATAT
88601	AAATATATAT	TATATATTAT	ATATATAATA	TATTATATAA	AATATATATA
88651	ATATAAAATA	TATTATATAT	TATATATATT	TATATATATA	AAATATATAT
88701	ATATGGGGTC	AGGGTCTCAC	TCTGTCAACC	AGGCTGGAGT	GCAGTGGCAT
88751	GATTTACAGT	CACTGGAAAC	TCTGCCTCCC	GGGTAAAGT	GATTCTCCGC
88801	CTGCCTCAGC	CTCCCGAGTA	GCTGGGATTA	CAGGCGCCCC	CCACCATACC
88851	CAGCTAATTT	TTGTGTTTAT	AGTAAAGTAC	AGTGTTCAC	CATGTTGGCC
88901	AGGCTGGTCT	TAAACTCCTG	ACCTCAGGTG	ATCCATCTGA	CTCAGCCTCC
88951	CAAAGTCTCG	GGATTACAGG	CATGAGCCAT	CACACCTGGC	CAATAATATT
89001	GCAATATAAG	AATGGTATAA	AAAGACACTT	TGATGAGTTA	GAGTAGTTCT
89051	TAGCGCAGAC	AATATGCAAG	ATTCTAAGCC	ATTAGACATT	TGTAGACAGA
89101	ATATCTAACA	GTGTAAAATA	AATAACACGA	AGATTCATTG	GCAATGAGAA
89151	ATTGACTTTT	TTCAATCATA	TTAGATGACA	TTAAAACCAT	TATAAAATTT
89201	ACTGTTTTGT	ACATAATAAA	GGATCATAAT	GTAAAACAAC	TTCATTAAAA
89251	GTTTGACAAA	TTAGGCATAT	AAATAGGCAG	CATGTTGACC	AGTAAACAGA
89301	AAATACACTT	TTCAAAGACC	AAACAAAATT	ATTTTTATTT	ATTTATTTCAT
89351	TTATTTATTT	ATTATTGGTG	GATGAGCAGC	TTTATTAGCT	GGGGATATAG
89401	TGGGGTCCCTC	TCCCTGGGAG	GTGGGGTCTT	TCACTGGTCA	CTCCCGGCAG
89451	TGGTCCAGGA	GGCGCCAGGC	AGTTCAGTGC	TGGGCTTAGC	TGGGGGCTGA
89501	GCCTTGAAGA	AGGCGAACCG	TGCAGGGAAG	TAGTAGCTGT	GGGGTCTCAC
89551	CTCCCGCTCC	GCCCTGCTGC	ACTGGGTCTC	CTGGTGCTCC	TCAGGGTCCC
89601	GCCGAGCCTG	AGTCTCTATA	GGACAGTGGC	CCATCCGGCC	CGAAACCTTC
89651	TCCTCAGAGC	CCAGTTTGAC	GCAGGCCAGG	CATTTCCACT	TCCTTCCCTT
89701	GGGATGGACT	TCGCACTCGT	GTTTCTTCCA	GTCCTTCCGC	CGGCCGCTTG
89751	TCTGCCTGAG	CTTAAATTCC	AGTTTCACAA	ATGTTCCAGC	TGGGAAGGAC
89801	GTATCCACCG	CGCCGTCCAC	ACCGTTCTCC	CGGAAGGCC	ATGCCGGGGA
89851	GGGTGCATTG	TCCAGGGCT	ACCTGCAGGC	CCCGGAGCTG	GGCCCCGGAG
89901	CTCGGACCCG	CCTGCCTCCC	CAGCGCCCCC	CGCGCCCACC	CACGGGGCCA
89951	GCAGCATCCG	CAGCCGTGGC	TTGCTTCTGC	GGTCTCTCAC	TCTGGCCCTG
90001	CGAAGCTCCT	GTGCACCGCT	CAGCTCTCTG	AGCCCGCTGG	GAGGTGCCTC
90051	CTCCCTGCT	CTTCCCCTGG	GTGGCTATGC	CCACAGAACT	CTGGGCAGAG
90101	GTCAAAGAGC	CAGGAAATGT	CTCTTTCTCC	AAATTGACTT	TGGTGTGCGC
90151	CTGGTCTCTC	CCACTCCCCTC	CTGCCCTGTC	CACACTGTTC	CCTGGGGCCC
90201	GCAGGTTTAG	CAAAGTTCCC	TGCCCCCTGC	CTGGGCCAGG	AAGCAGTCTT
90251	GTTGCCCACT	CCCACCCTTC	AACCCTTTTA	TGGCCCATTC	TCTCTCCCCA
90301	CTGGGTCTCC	CACACGACAA	CCCCTCCTCC	CTACTGTCCC	CGGAGCCCTT
90351	CTCTGGTTCT	CGCGCTCAGC	CTCTTCCCTG	ACTGCTTCTC	CATCTCCATC
90401	CTGAATCTCC	CAGCTCCAGT	AGGGTGCCCC	CCAATCCCAG	GGCCCAGGCA
90451	AAACCAACAA	AATTATTTAA	AATGGGAATA	TTTGAATTCC	ACTGAATTCC
90501	TAAAAGCAGA	AACCCATCTG	GTTATATTTT	AAAGAATTAT	GAATTAATAA
90551	TAGCAACTAT	CAATTTAAAG	TGTAACCAGG	GTTAAGAATA	CCCACCATT
90601	TAACAACAAC	AACAATGAAA	GCGTGTTATA	GCTAACAAAC	TAGTTCCTGA
90651	AAGTTGCAGG	ATACAATATT	AACATGAAAA	TCAGTTGCAT	TTGTATACAG
90701	TAACAACAAA	ATATCTGAAA	AAGGAATAAA	GAAAACAATT	CCATTTACAA
90751	TATTATCAAA	TAGAATGAAA	TACTTAATT	ATTAAATAGA	ATGAGTTTAA
90801	CCAAGAAAAA	TAAAGATCTG	CATACTGGGT	CGGGCGCGGT	GGCTCATCCG
90851	TGTAATCCCA	GCACTTTGGG	ACACCAAGGC	GGGCGGATCA	CGAGGTGAGG
90901	AGTTCGAGAC	CAGGCTGTCC	ACATGGGGAA	ACCCCGTCTC	TACTAAAAAT
90951	AAAAAAAAAA	TTAGTCGGTG	GTGGTGATCT	CCTGTAATCT	CAGCTACTCA
91001	GGAGGCTGAG	GCAGGAGAAT	CACTTGAACC	CAGGAGGCAC	AGGTTTCAGT
91051	GAGCCAAGAT	TGGGCCACTG	CACTCCAGCC	TGGATGACAT	AGTGAGATTC
91101	CATCTCAAAA	AAAAAAAAAA	AAAAAAAAAA	ATCTGCATAC	TGAACACTAT
91151	GAAATGTTGA	TGAAAGAAGT	AGAAGAATAG	GCCAGTTGCG	GTGGCTCACG
91201	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAG	GTGGGTGGAT	CACGAGGTCA
91251	GGAGATTGAG	ACCATCCTGG	CTAAAACGAT	GAAACCCCGT	CTCTACTAAA
91301	AATACAAAAA	ATTAGCCAGG	CGTGGTGGCA	CGCGCCTGTA	GTCCAGCTA

FIGURE 3, page 29 of 41

91351 CTCGGGAGGC TGAGGCAGGA GAACTGCGTG AACCTGGGAG GTGGAGCTTG
91401 CAGTGAGCTG AGATGGCGCC ATTGCACTCC AGCCTGGGTG ACCGAGCGAG
91451 ACTCCGTCTA AAAAAAAAAA AAAAAAAAAA AAAAAAAGC AGCAAGCAAG
91501 CAAGCAAGCA AGCAAGAAAG AAGTACAAGA ATACGAAATG TGAAATATAT
91551 CCTGTGTTCA TGGATTCTAA AAATTAATAT TGTAAAAATA TCTATACTGG
91601 ACAAAGTCAT CAACAAAGTT AAAGAAATTT CTATCAAAAT TTTAATGCCT
91651 TTAAATAAAG TGTAGAACAA ACAATTCTAA AATTAGTATA GAGCCATGAA
91701 AGACCCCAAA TAGGCAATA CTGTGAAGAA CAGAAAGGCT GAATGCCTCA
91751 AACTTCCTGA TTCAAACCTG TATTACAAAG CTATAGTCAT TAAAGTAGTA
91801 TAGAACTTAC ATAGGAACCA CTGAAACAGA ATAGAGGACC TAGAAATAAA
91851 TTCACCCATA TGCAGTCAAC TGGTCCTACA GAACCAGGAA AAGATAGGGA
91901 CATCAAGAAG TGGTTTAGAA AAAACTAGAT ATGCACACAC AAAAAGTGAA
91951 ACTTTCCTTAT ATCATCACAA AAAATGAGTT TAAAAATAAA GGCTTAAACA
92001 TAATAAAGT AATCAGAGT CGTCTTTAAA AAATAGGGAA AAAGCTCCTT
92051 CACCCCGGTC GTGGCAATGA TGTTTTGGAT TCTACACAAA GAACACAGGC
92101 AACAAAAGCA AAAATTTAAA AAATGGAAC ATATCAAAGT TTCTGCATGA
92151 TAAAAGAAAG AATCAAGAAA ATATAAAGAC AATATATGGG ATGGGAGAAA
92201 ATTTTCGTAA ACCATATGTA GGATAATATG TTGCTATTCA AAATATACAG
92251 AATACTAATC AATATGAAAA AAGCATCCAC AGGAGAACAA AACAAAAACC
92301 AATTCCTGA TTAATTGGGC AAAATATTCA TTTTCCAAA GACATACAAA
92351 TGGCCAGCAG GTATATGAAA AGTTTCTCAA CATCACTAAT TATCAGTGTA
92401 ATTAATAATCA AAATCAAAT GAGAAATCAC CGTATCATGG TGTTAGGATA
92451 ACTATTATCA AAGTGTCAAA AGAACAAAGT GTTAGGGTGC ACAGAAAAGA
92501 CAATATTTGC ACACAGTTGC AGAGCATGTC CTTTGGTGCA GCCATTACAA
92551 AAAAAAATC CAGTATGGAG TTTCTTTAAA ATTTTAAAC TTGAAGAACC
92601 ATTAATCCCA ATTTGGAGAA TATAGCCAAT GGACATAAAA TTAAAGTATA
92651 CCGCAGGCG TTTGCATGCC TCTGATACAA ATAGATGGAT AAAGTGTAAG
92701 ACAGAGATAA TTTAGCTTTT AATAAGGAAT GAAATGTGTT TAGTTACAAA
92751 AATATTGATG AACCTTGAAG ACATGATGCT AAGTGAGATC AGCAAAATAC
92801 AGAAAGGCAA ATATTGCATG ATCTCATTG TATGTAGATA TATTAAAAAA
92851 AAGAAAGAAA GCGGAGAGAAG GGTAGTTTGC ATGGGCTAGG AAATGGGGAA
92901 AGGAGGAGAT ATATCCATTG AAGGGTGCAT ACCTTCAGTT ATATAATGAA
92951 AAAGTGCTGG GGACCTAATG TGCAGAATGG TGACTATAGT TAATAATAAC
93001 GTGTAGTTGA AATCTGTTAC TAAAGTAGAC CTGAGGTGGT TTTACTACAC
93051 ACACCTGAAAT GTATAAAGTA ACTATGTGAG GTGTTAGATA GGTTAACCAG
93101 CTTCACTGAG ATAATTTAAA GACGTATACA CATCTCAAAG CACTCTATTG
93151 TATACCTTAA ATAAATACAC TTTTCAATGT GTAAATGTGG AAAAAAATTA
93201 ACAGTAGTCA GCAGGTCACA TCTAGCCACA TGTAACCTTT ATTTAAAATT
93251 GTTGGCCACT CTTTCTGGCT CAACCCGGGA ACAACCGGAG CACTTCTGGC
93301 CCCTTGGACT TTGACGCTCC TCCCCTGTT CCTGTACTGG GGAAGATATG
93351 GATAGTTCCC AGGGGTGGGT GGGCGCAGTG GCTCACGCTT GTAATCCCAG
93401 CATTTTGGGA GGCCAAGGTG GCGGATCAC TTGAGGTCAG AGGTTGAAGT
93451 CCAGCTAGAC CAACATAGTG AAACCTGTC TCTACTAAAA ATAGAAAAAT
93501 TAGCTGGGTC TGGTAGCCTG CGCCTGTAAT CCCAGCTACT CAAGAGGNNN
93551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
93601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNGTG
93651 TGAGGCAGGA GTATTGTTTG CACCTGGGAG GCAGAGGTCG CAGTAAGCAG
93701 AGATCGTGTC TGTGCTCTCC AGTGTGGGCC ACAGAGTGAG TCTGCGCTTT
93751 AAAAAAAAAA TATAATATAT ATATTATATA TTATATATAA TATATATATA
93801 ATATATTATA TATCTAATAT ATATATTATA TATAATATAT ATTATATATA
93851 TACTATATAT ATTATATATA TAATATATAT ATAATATATA TAATATATAT
93901 AGTATATAAT ATATATATTA TATATATAAT ATATATTATA TATAATATAT
93951 AATATATAAC ATATATATTA TATGTTATAT ATATATGTAT GTATGTATTT
94001 CCCAGGGTTT TTTCACATCC CAGACTGTGC AGATCAGGGA GGGCCATCAG
94051 CAGTCCCTTT ACTAGTTGCC CACAGACCCG TTTGGCTCCA GGCAATGCAT
94101 ATCAGGGCAT CCAGGTGGGA GCCACAGCAG CCAGCAGGGA GGAGGCTGCC
94151 TTTGGCTGCC TGCAGTCTGG TGGCCTCTGG CTCCGCAGGT GTCTGTAAGG
94201 CCCAGCGCA GCCCTCCTC ACATTGCCTG TGAAGGCAAT GTAAGTGCAG
94251 AACATACTGA GGAGGAAATT GAGGAAAAAA ATGTCCCCCA TATATTAGAA
94301 TAATTGTCAT TAGATCGCTT ATGCTGCAGA CAGGGTCACT GTTTATCATT
94351 ACTGCTGTGA AACCCTGCTAC AATTGGAAGA GAAAATGATC TAGGGCATAC
94401 CCTTTGATTC CCATAAGTTG GTGTCAAGTAG GTTTCATGCA GAAATTTATT
94451 TTGACCATGA TTTACAAAGT TACGTCCTTC TAGATCAAGG CAGTCAAAAT

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94501 TGAACAACTG TTCATGGAAA ATGAATTGTT CAGCTGAAAA CTAAATGAGA
94551 CCCTTTATGTA CGTGAGCATA GACATAAATT TAAAATTGGA GAGACTGTGT
94601 CACCCTTTCA CATTCAACCTT GGCAGTGATA GCTGTGATGG CTGTGAACCA
94651 TGGCAGGTTA GAACTCACTT TTGCTTTGAT AAGAAAGATG AATCTTTTGT
94701 TGGTCTACCA CTAAGTAAAG AGGAAAATGA GTTGGAATA AGTAAACAAT
94751 TAAAGAAAAT ATGACTAAAA TGGGGTTTAC AGAATATAGA TTATGAACAT
94801 GAATAGACAC TGAATAATCT AAAATATAAA GATAGAGCTG GAAATCATAG
94851 TGAGCAGATT GGAAGTGAAG GAACATTCTA GAGAGATGTT GCTCCTGCAT
94901 CTGTTTCATTC TGAAATTACT GACAGTAACA AATGTCAGAA GATGTTGGAG
94951 AAGATGGGTT GGAAGAAAGG AGACGGCCTG GGAAGGATG GTGGGTAATG
95001 AAATCTCCGA TTTAGCTTCA GCTTCAGTGA ACATATGGAG GCTTGGGGAC
95051 AGGCAATCCA TCCTCAATTG AAGACGTTCA GCTTCTCTGA AACAAAAAAC
95101 AACCTGGGAC AAAGCGTGAG AGAGGTTTGC TGAATTTTC CCAGAAACCA
95151 AACCTTAAAA AGATGACCTA GGTACCAGGC CTTGGATAAA AGGAACTGTA
95201 CAGTGAAGGT TAATCATAGA AGAAAACTCA AGCTTTTCAA AAAATAGAGT
95251 TTGGAACTC TTTATTTTAT ATATATTTGC AGTACTTTTC TCCCCAAAAG
95301 AGTCTGTGGC ACAGAGGAAC AGTGTACAG TTTACCCCTT CTGATTCAG
95351 AAATGTGTAA TAAAGTTTGG TTTGCAAATT TTAATAAAC TTTTATAAC
95401 TAATAAATAT TGAATCAAGT TATTCAGTAA GTGGACTAAA GTTTACAGGT
95451 TAAAGATGAG TTTATCAAAC TTCCTTATTT TATCTTGTC TTTATGACAT
95501 CCATATAAGC AAAAAGCCAC ATAAGCAAAA CTCATAACCA CTAATGACTT
95551 AAATGTACAT TTGTCTGTGT GTCCATGTAT TCACAGTAAG GTGCACAGCA
95601 AAAGAAACAA CAAAAGTTTA TAAAAATAAA TCTGACTACA TGCATCATTG
95651 TTTATGCCCT TTAGAACTA GATAAAAGAA CCTCTTATAC TTGAAATAGC
95701 CTAAATATTA TTGAAGAACA AATGAACAGC TGATATATTG TAGAAAAATTA
95751 GTCAGTGTTT TCTTTTTTGA AGAATCCGTT TATTAGTACT ATATCTTCAG
95801 TATTTATATT GGTGTGTTTC ATAGCTAATG TGATATTTAG ATATGAACAA
95851 CTGAGTACAG TGTGAAATA GTGTGCTGGC ATTTGTAGTT TTCATAAATA
95901 TTATTGCAGG CAGTGGTGTT GTGCCACAGA AATCTGATTT CTAGTACATA
95951 AGGATTACTT AGCCAGGGCC TCATGTTTAA GATATTTAAT GAAAATGTCT
96001 TCAACTGCAA TAAAAACATT GTAACATTAA AAATACTCTT TTCAATAAAT
96051 TCTAAATTAA AAAATTCAAA TGATACCTTT TATGGAGTTA GGAAGTGCT
96101 AATAAGGTA AATGGCAACT GAAGCCAAA AATGTAAATT CAGGTAAATA
96151 CTTTTACCCT TATTAGTTGT ATGTTAAAGG AAACAATAAT AAACAATAAT
96201 TCTGACCATA TACTATTTAC TGCAGTAAAG TATTTGAGAA ATTTGTGCAT
96251 AATACATAAT TAATTTTCTA ATGGTATAAA AGTAATCACA TTCTACAAAT
96301 TATTACAACA CGGTCTATTG AAGACAGCGG CATTTCAAGT GAAGAATCTT
96351 AGAGTTTCTC ACGAGGCAGT GATATATGCC ATATGAAATC TAGGTAAAT
96401 ATTTTACTCA TGTATGCAAC AGTTGATATT TCTGCTTTCC AGGAAAATAA
96451 CATGCTTTAA AAACTTAATG CAGGTAACATA AAATCAACCA GAAGTTATAA
96501 GAACTCACAC AATGACTAAT ATAGTTGAAA GAAAATTATG AAAACTTCTC
96551 AGGACCAGAA GTAAATAAAG GGTATAATCC AGAGAAGTAT AGACCTAAGA
96601 GGCCAGTGCT CCATTCAGAT GCATCTGATC ACAAGGACAT CAGATCCACA
96651 TGGGTTGTTC AGCTTCTGAC AAAGCAAATG GAATAAACAA AGAGAACTG
96701 CCTGCAGGCA TCCAGAGTGT GATGTCTCCT ATATGTGAGA GCTAAACTAT
96751 AAATTATGTT GCACACAAGG AGAAGAGCTA TTAGAGTGAA GCATTAAAT
96801 ATATGGCACA TAAACTCAG ATATGAGGAT TATAATTACA TGTTTGCCAA
96851 TATAATGAAA ACACAAGAAA CCGAAATAAT GTGGAAAAA CTATGAGCTT
96901 GTCAAGTCAT ATTTGGAATA GAGGCGAATG GAAAGTAAAC TTGAAAATTT
96951 GGTAAACAA CTTAATGTAC AGCATACAAA TTACACATTG AAATAGACTG
97001 AGATGGTGAG AGGACTAGTA AACTGGAATG CTGAGCACA TTAATGTAGT
97051 AATATACCTT TTAGAAGGCA AATTAATACA AAATACAAAT ATATATGAAA
97101 ATTAGATGAG AAGAAATGAA AAACATTTAA TTGCTTTACT ATACTATATA
97151 AACAGGAGGG CAATATTCAA AAAATCAGT GACTCATAAT TTTAGAAAT
97201 TGGAAACCAG GCATGAATCC TATAAAAGTT TAGAGTGTA TGTGTGAGAA
97251 AAGATAAATT AAGAAATACT TAAAAATAAT AATGATTTTG GTTATTGTGA
97301 ATACTGCTTC AATAAACATG GGAGTGCAAT TATCTTTTGG ACATACTGAT
97351 TTTATTTTCT TTTGATATAT ACCCAGTGGT GAGATTGCTG GGTATATAT
97401 ATGGTAGTTT TATTTATAAC TTCTTGAAAA ACCTCCATGC TGTTTTCTCT
97451 AATGGTGGTA CCAATTTAAA TTCTCACCAG CAGTGTATAA GTGCCTATTT
97501 ACAGATGAAT GAAGAAAATG TTATACATAC ACACAGGCAC ACATACACAC
97551 ACAGGAATAA TGCTCAGTCA TAGAACAGAA TGAACCTCTG TCATTTATGT
97601 GAACATGGAT GAACCTAGAG GACATTATGT TAAGTGAAAT AAGCCCATCA

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97651 CAGAGAGAAA AAGACCACAT GATGTCACTC ATATGCAAAA TCTAAAAAAG
97701 CAGATCTAAT AGAAGTAAAG AGTAGAATGG TGGTTACTAG AGGCTAGGGA
97751 GAGTGATGGG ATGAAGGAAT GGGGAGAGGT TTGTCAAAGT TACAAAGTTA
97801 CAGTCAGGGA GAATAAATTC TGATGTTCTA TTACACAGTA GGGTGACTAT
97851 AGCTAATATA ATGTACTATT TATTATAACA CAGCTAGAAG AGAGGTTTTT
97901 GAATTTTAAT AGCACAAATA AATTATAAAT GTTTACACTG CTAGATATGC
97951 AAATTACCCT CATTGGGTCA TTTTACAGTG TAAACATGCA CTGAAACATC
98001 AACTGTAGC CCATAAATAT GTACAATTAT TATGTGTCAA TTATACATAA
98051 AATAAATCTT AAAAAATAAT AATGATCGAA TTGCATAAAA TCAAAACGAA
98101 GAAAAACTCT TAAAAGTAGT GAGATAGAAG ACAGCTAACC TGTGAAGCTG
98151 AGGGAAAACA CTTACCTCTG TATCAAGTCA GAAAACAGAA AAATTAATAT
98201 CAGTAAATA TTTAAAGCTT CTGGACAGCA CAGAAATCTA TTAATAGAGT
98251 GAAAAGACAA CATATAAAT GAAAAAAAT ATGTGCATCT GGCAGGGAGT
98301 TAATATCCAA AATATATATA TGACTCAACT CAACAGCAAT AAAAATCAAA
98351 AACCCAACTA AAGAGTGAGC AAAAAACCTG AATAGACATT TTTCCAAAGA
98401 AGACACAAAG AAATGCTCAA CATCACGAAT CATCTGGAAA ATGCAATCCA
98451 AAACCACATG AAATAGTACC TCACCCCAT TAGAATGGCC ATTATCAAGA
98501 AGACAAACGA TAACAAGGTT TGGATGAGGA TGTGGAGAAA AGGGAACACT
98551 TATACACTGT TGGTGTGAAT GTAAATTTAG TACCTTTTGA GATTCAATTA
98601 TTTATTGATA AGAAACCTGC ATGGAAAAT ATGCAGGTTT CTCCAAACAA
98651 AAAACAAAAA CCTAAAAATA GAACTACCAT ATAATCCAGC AATTCCATTA
98701 TTGAGTATAT ATCAAAAGGA AATAAAATTA GTATATTGAA GAGATAGCTG
98751 CTCTCTCATG TTTATCATAG CTCTATTGAC AACAGCCAAG ATATGGAATC
98801 AATCTTGTGT CCATCAGGGA TAAATGGATA AAGCGAATAT GGTGTATACA
98851 CATAATGGAA TACGATTTAA CCATAGGAAA AAAAAATCC GCCCTTTGGG
98901 AGGCCGAGGC GGGCAAATCA GGAGGTCAAG AGATCGAGAC CATCTTGGTC
98951 AAAATGGTGA AACCCCTTTT CTAATAAAA TACAATTAGT TGGGCGTGGT
99001 GGCACGCGCC TGTAGTCCCA GCTACTCAGG AGACTGAGGC AGGAGAATCG
99051 CTTGAACCCG GGAGACGGAG GTTGCAGTGA GCCAAGATCG CGTCACTGCA
99101 CTCCAGCCTG GCGACAGACG TTCCGTTTCA AAAGAAAAAA ATAATATTAA
99151 TAAAAAGAAT AAAATCCGGC GCTGCGCGGT GACATCAGTC TCTGTCGTTA
99201 ATGCCTCGCG CCGGCTACCG TCCTGCGCAG TCTCTTTCTG AGGACCCCCC
99251 CCCCACCTCT CCGCCTTCCA ATAAGGAGTT CAGGTTTTCG GGTCCGCGTG
99301 GTTGCTGTTC CTGCTGCCAC AGGTTGGAAC TGGAGATGCC TCTTCCTTCT
99351 CTCAGGACAG AACCATGAGC CTAGCGGCAG CGCCGGTTCT CGAAGCTCCC
99401 CCTCCGCCAA CGGGCGCCTC CTCAGAGCCG TCCGTGCCCC CCCTGCCGGG
99451 AGCTGACCCG CAGCGCAGTG CAGAGTTGCT CCTGTTGGCG GTGACCAGGG
99501 AGGGACTGGA GCGGCGGATC ATCTCCAGGA AGCGGGCTGA GTAGGAACTG
99551 CAGCCGCCAC ATCCTCTCTT TACCCGGGGA TGTGCAGGAT TACCGTGAAA
99601 TCATCACTCG TCATCCTCGC AATTACCAAT GGGAAAATTG GAGTCTAGAA
99651 ATTATTGCCT CCATTTTAGC CCACCGGTTT CCCAGTAGCT GTATTGGGGT
99701 GATGAAGTGC TCCGAACAA ATGCGCTGCC ATGATAGTTT TCTGAAAAGT
99751 AACATGTTTG GTTTCCAGAA ACACAATACA GACTCTGGAG CTTTAAAGCA
99801 CCTTTATATG TTATTAGTTA ATGCTTTTAA GTCAGAGTAG TTTATCAAAG
99851 GAAAATTTGA ATGATTGGAA TAAGGACTCC ACAGCATCTA ATTGTAGATG
99901 TCCAATTCTT CTCATACTAC AAATCATTTT CAGGAAGGAA AAGATAGGAC
99951 CTTTGAAAAA TCTGATGGAT CGGCCATGTG TTTTATCCA CCATCACTAA
100001 ATGATGCATC TTTTCTTTT ACTGGATTCA ATAAATGTGT TGTTTTGAAT
100051 CAGTTTCTTT GAATTGAAAG AAGCCAAGAA AGACAAAAAC ATAGATGCTT
100101 TCATTAAGAA CATAAGTACA ATGTATTGGC TGGATGGTGT TCATTCCGGA
100151 GGAAGGAATA CTGGAGTTAC TTATCCACAA GTCTTGAAAG AATTGCACA
100201 AACAGAATT ATTGTTTACA CCCATGGAAC ACTTTACCAA GTATGTGATC
100251 TAATGAGATC TTGCATTGGA AAGGAGCAAA ATAAATTTTT TAGATACTTG
100301 GGGATATTGG TATGCTGGTG AGTAGCTGAA TTCATTTTAC GAAGGAAGCT
100351 CCCTACATAG AGAATCCCTT TCAGAATTCA TGAAGTGTTT GAGACTACAA
100401 GTATATTAAT GTACTTGTTT AGCGGAAGAG CATAAGCACT TTGAGTGTTA
100451 TAAATTCAGA TAATGGAATG TACTTCATAG ATGTATTGTC AGTTTGGGGG
100501 TATGGAGGGA AGCACACATT CCTGAAAAAT GAGTGTAATG TGC

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FEATURES:

Start codon: 1000
Exon: 1000-1062
Intron:1063-2440
Exon: 2441-2514
Intron:2515-3016
Exon: 3017-3171
Intron:3172-33878
Exon:33879-33959
Intron:33960-39894
Exon:39895-40002
Intron:40003-50367
Exon:50368-50398
Intron:50399-50736
Exon:50737-50886
Intron:50887-53571
Exon:53572-53605
Intron:53606-65379
Exon:65380-65613
Intron:65614-74191
Exon:74192-74299
Intron:74300-79441
Exon:79442-79459
Intron:79460-99355
Exon:99356-99544
Stop codon: 99542

336000014324295

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
948	T	-	Beyond ORF(5')			
1149	G	A	Intron			
4199	G	C	Intron			
4352	T	G	Intron			
6493	A	G	Intron			
14047	T	G A	Intron			
14136	G	T	Intron			
14238	G	A	Intron			
14260	T	G	Intron			
25736	C	T	Intron			
26321	G	A	Intron			
31359	A	G	Intron			
35098	T	G	Intron			
40532	C	G	Intron			
41706	A	G	Intron			
51095	G	C	Intron			
53101	G	C	Intron			
54556	G	C	Intron			
61872	-	T	Intron			
62172	G	C	Intron			
62860	A	C	Intron			
67086	C	A	Intron			
67621	A	C	Intron			
70582	A	T	Intron			
74175	C	-	Intron			
74478	T	C	Intron			
77092	T	G	Intron			
77328	T	C	Intron			
77385	G	A	Intron			
77947	C	T	Intron			
79395	G	C	Intron			
81111	-	C	Intron			
81610	G	A	Intron			

Context:

DNA
Position

948 TGTGTCCTCCTGAATCTTAGTGGCCTTCTAAAGGCGGGTGTGATCAGCCATGGGTATCAG
AGACACTGGAGTCCAGTAGCTGCTAGGTGGGACACGGGCACAATTTCACTTGCAGACCAG
CTGCACGGAGTGGATAAAAGAGAGAGTTCCTGTGTGGGAATCTCCTTTGGTGGATCATCAGG
GAGGTGAAGTCTTTGTCATAGCCTCATATCCAGCTTGTGTGATACCAATTCAGTGAAGC
TGGAACAAGCTGGCACTGCTCAAACAGGCCTACCAAGACATCATGTTTTTTTTTTTTTTT
[T, -]
CCACCAAACCTGGACCTGAATGGGGATGTGGACACACATAGAGTCCAGAGGATGGGACCC
TGGTCAGTGGTGGTGGTGTGCGGCATGAAGCAGCTGGGGCAGGCCCTCCAGGTGGGA
GGAGGAGCCAGCCTCTCCTGTGGGGTCCTGGGCAAGTCATTTCCCTCCTTGACGCTCTGT
TTCCTCATCTGGAAAATCCAGGAAGCCTGTTGTGCAGTCTCAGAGGGTCATGATAAGGT
GCAAAGGAGGAAGAAATTTGAGAGTCTTGTGCCTTCCTCTTCTGAGAGGGATGATGG

1149 CCTCATATCCAGCTTGTGTGATACCAATTCCAGTGAAGCTGGAACAAGCTGGCACTGCTC
AAACAGGCCCTACCAAGACATCATGTTTTTTTTTTTTTTTCCACCAACCTGGACCTGAA
TGGGGATGTGGACACACATAGAGTCCAGAGGATGGGACCCTGGTCAGTGGTGGTGGTGGT
GTGCGGCATGAAGCAGCTGGGGCAGGCCCTCCAGGTGGGAGGAGGCCAGCCTCTCCTG
TGGGGTCTGGGCAAGTCATTTCCCTCCTTGACGCTCTGTTTCCCTCATCTGGAAATCCA
[G, A]
GAAGCCTGTTGTGCAGTCCCTCAGAGGGTCATGATAAGGTGCAAAGGAGGAAGAAATTTTG
AGAGTTCTGTGCCTTCCTCTTCTGAGAGGGATGATGGTGAGAACAGTGTGGATAACCA
CATGCAACTGAGTCCCCAAAAGGCCCTGTGAGGAAGGTGTGTTCCCATCATGCTTCCCA
GATGAGGAAACAGTCTCAGGGAGGCCCTGGCTGCATGCCCAAGGGTTACACACACACTGAA
TGTTGGAGCTGGGAGTAAATCTAGAGTCAGGGCTCACTGGAGGTGGTGGGAGCATTGCAC

4199 AATGTGGATGATGGTGCAGAACAACTCTGAGCATGATTAATTCTCTGACTTGACGTTA
GAAATTGTTAAAATAGTTAATTTTATGTATATTTTACCACAATGTAAAAAGGAATTTT
AAATGAACAGACTGTAGATACATGCAACAGCATAAATGAATATCACAAATATAATCTTGC
ATTTAAAAATTGATGTAAAAGTATCCAACTATATAATTTTCAATTTATACTAAATCCAAAA
ATCAAACTGACATTCTTGCTTTCACTAATGGGAATTAGCTAGTTAACTAACACTCTCA
[G, C]
AGAGAAAAATGATGAATCCTAGATAAAATAGTATATATCATTATAAACACTTCTATATAT
AATACATATATGAGATATGTGTGTATAAGAAGTGAATGAGGATGTCCCCTGTGCCCTCCT
TAGGAGAGACAAGAATTGAAGTTATAATCCAGGCCAATTAGCACTCTCTTTAAAAATCAA
CACTCTTCAAAGGGACACAACAGAATCCAGAGTCTCTATAACTCTTGATACAGTCTCTT
GTACACAATTTTCAAATTCGTGAGATGGGTGAAGACACATGAAAATGCAATACATACACA

4352 AAATGAATATCACAAATATAATCTTGCAATTTAAAAATTGATGTAAAAGTATCCAACTAT
ATAATTTCAATTTATACTAAATCCAAAAATCAAACTGACATTCTTGCTTTCACTAATGGG
AATTAGCTAGTTAACTAACACTCTCAGAGAGAAAAATGATGAATCCTAGATAAAATAGT
ATATATCATTTATAAACACTCTTATATATAATACATATATGAGATATGTGTGTATAAGAAG
TGAATGAGGATGTCCCCTGTGCCCTCCTTAGGAGAGACAAGAATTGAAGTTATAATCCAG
[T, G]
CCAATTAGCACTCTCTTTAAAAATCAACACTCTTCAAAGGGACACAACAGAATCCAGAGT
CTCTATAACTCTTGATACAGTCTCTTGACACAATTTTCAAATTCGTGAGATGGGTGAA
GACACATGAAATGCAATACACACAAGATAAAAGGCAGGCAGTAGACATCTCCAAGAT
ATCCAAGATGTAATCAGCAGACAAGAATTTGAAGGCAGCTATTACAAGTATGCTAATGGA
GGCAAAGGAAAAATATACTTATAAAGGAACAGATGTGGAACCTCAGCAGAGAAATAAAA

6493 TCTTGAAACCAGGAGTTCGAGACCAGCCTTGGAACATAGTGTGAGCACCCCTCCGCCCCC
CAACCTTTTCTACAAAAAAGAAAGAAAGAAAAAATAGCCAGGCATGGTGGAGCTTGTC
TGTGGTCCCAGCTACTTGGGGGACTTAGGTGGGAGGGTCATTTAAGCCTGGGAGGTAGAG
GCTGCAGTGAGCTGAGATCAGGCCACTGCATGCACTCCAGTCTGAGTGACAGAGCGAGAT
CCTCTCTCTCTATCTCTTCTCCTCACTCTGTGTGTGTGTGTTGGGGAGAGGGGTGTGTGTT
[A, G]
TGGGTGTGTGTGTGAGTGTGTATGTGTGTTTATTATTCAAATGAAACAACATAATGAC
AATTATTTTTATTTTTATTTTTTTGAGACAGAGTCTCACTTTGTCAACCAGGCTCCAGTG
CAGTGGTGCGATCTCGGATCATTGCAACCTCCGACCCCGAGATTCAAGCAATTCATCTGC
CTCAGCCTCCTGAGCAGCTGGGATTACAGGTGCCCACTACCTTGCCCTGGCTAATTTTTGT
ATTTTTAGAAGAGGCAGGGTTTTGCCATGTTCTCCAGGCTGGTTTTGAACTCCTGAGCTC

14047 TGGAAGCCTCTGTCCAAATCTCCAGGCTATCTATGTGTGGGAAGTGGAGTCAGGAAAGA
CCCTAGAGCTTTGGAAGTGATCATTAAGAGAAAAACAAATCCCTGTAAATTAGAGTACAA
GGGAACATATTCATTAGCCACCTTTAGAGTCAGATGCTCAGGGCTGAGCTGGTGTGGGGG
AGTGTTCAGACCTGTGCATGCCTGGGAAAGCCTCCGATCATGTATGAATGGTGGGCTTC
TGGGTGCATGAGATTGAGTGCCCTTCTTGGCAGAGCACCACTGAGTGAACAATTGATTT
[T, G, A]
GGATCAAGCATATGGAGATCACTTTATTTTTGAATATCTCAAAGACAGAACTGAAAAGA
TTTTTTTGCACTTTGAAATTGAGTAAGGGTGTGAGAACTTCAGTAAAAAGTCACAGGA
GGAACCCAGAAGTCTTATTCATCCCCAGAAACCACCAAAATCCTGATCCAACTGTAAG
AATTCCTCGTAAAAATTTGATTTTTGAATAGGAACAGCTCCGGTCTACAGCTCCCACT
GTGAGCGATGCAGAAGACGGTTGATTTCTGCATTTCCATCTGAGGTACCAGGTTTCATCTC

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14136 GAAACAAAAATCCCTGTAAATTAGAGTACAAGGGAACATATTCATTAGCCACCTTTAGAG
TCAGATGCTCAGGGCTGAGCTGGTGTGGGGGAGTGTTTCAGACCTGTGCATGCCTGGGAAA
GCCTCCGATCATGTATGAATGGTGAGGCTTCTGGGTGCATGAGATTGAGTGCCTTCCCTT
GGCAGAGCACCCTGAGTGAACAATTGATTTAGGATCAAGCATATGGAGATCAACTTTAT
TTTGAATATCTCAAAGACAGAACTGAAAAGATTTTTTGCACCTTGAAATTGAGTAAGG
[G, T]
TGTCAGAACTTCAGTAAAAAAGTCACAGGAGGAAACCCAGAAGTCTTATTCATCCCCAG
AAACCACAAAATCCTGATCCAACTGTAAGAATTCACCTCGTAAAAATTTGATTTTTGA
ATAGGAACAGCTCCGGTCTACAGCTCCCAGTGTGAGCGATGCAGAAGACGGTTGATTTCT
GCATTTCCATCTGAGGTACCAGGTTCTCTCACTATGGAGTGCCAGACAGTGGGCGCACG
TCAGTGGGTGTGCGCACCGTGCAGGAGTGAAGCACGGTGAGGCATTGCCTCACTCACGAA

14238 CTGTGCATGCCTGGGAAAGCCTCCGATCATGTATGAATGGTGAGGCTTCTGGGTGCATGA
GATTGAGTGCCCTTCCTTGGCAGAGCACCCTGAGTGAACAATTGATTTAGGATCAAGCA
TATGGAGATCAACTTTATTTTGAATATCTCAAAGACAGAACTGAAAAGATTTTTTGGCA
CTTTGAAATTGAGTAAGGGTGTGAGAACTTCAGTAAAAAAGTCACAGGAGGAAACCCAG
AAGTCTTATTCATCCCCAGAAACCACCAAAATCCTGATCCAACTGTAAGAATTCACCTC
[G, A]
TAAAAATTTGATTTTTGAATAGGAACAGCTCCGGTCTACAGCTCCCAGTGTGAGCGATGC
AGAAGACGGTTGATTTCTGCATTTCCATCTGAGGTACCAGGTTCTCTCACTATGGAGTG
CCAGACAGTGGGCGCACGTCAGTGGGTGTGCGCACCGTGCAGAGTGAAGCACGGTGAGG
CATTGCCCTCACTCACGAAGTGCAAGAGGTGAGGGAGTCCCTTTCTATTCAAAGAAAGG
CATGACAGATGGCACCTGGAATCGGATCACTCCACCCGAATACTGCGCTTTCCGAC

14260 CCGATCATGTATGAATGGTGAGGCTTCTGGGTGCATGAGATTGAGTGCCCTTCCTTGGCA
GAGCACCCTGAGTGAACAATTGATTTAGGATCAAGCATATGGAGATCAACTTTATTTTG
AATATCTCAAAGACAGAACTGAAAAGATTTTTTGCACCTTGAAATTGAGTAAGGGTGT
CAGAACTTCAGTAAAAAAGTCACAGGAGGAAACCCAGAAGTCTTATTCATCCCCAGAAA
CCACCAAAATCCTGATCCAACTGTAAGAATTCACCTCGTAAAAATTTGATTTTTGAATA
[T, G]
GAACAGCTCCGGTCTACAGCTCCCAGTGTGAGCGATGCAGAAGACGGTTGATTTCTGCAT
TTCCATCTGAGGTACCAGGTTCTCTCACTATGGAGTGCCAGACAGTGGGCGCACGTCAG
TGGGTGTGCGCACCGTGCAGGAGTGAAGCACGGTGAGGCATTGCCTCACTCACGAAGTGC
AAGAGGTGAGGGAGTTCCCTTTCTATTCAAAGAAAGGCATGACAGATGGCACCTGGAAA
ATCGGATCACTCCACCCGAATACTGCGCTTTCCGACGGGCTTAAAAAATGGTGCACCA

25736 AAATCATGTACATAGATATTATAATTTTTCAAATGCTTGGAAATGTCAAATTAAAAATTAT
GGTTGATTGTATTAAATAGATACATATATGATAACATAAAAAATATGAAGAAAAAGTAAAT
ACCAAAATAAAATGGCTCAAATAATTAGAGATTAGACAATTAATTAGACAATAATTAGATC
AAATACAATCAACTCGAATTTATTTAATTAGAGCAGATGCTAACTTAATCAGCGCTGAT
TCCTGAGGTAGCAAAAAGTCTAGGTGGAGAGAGAACTTACCCCTTTTCTTACCCTTCCT
[C, T]
GGTCATCCTGGGAGCTCCACTTTCCTCTGTAGAATTTATTCAGCCTCCTTAGTAAACATG
GACTTGGTCCCAACAGGTAACCCAACTGACCACAAGAAAAGCAGCCTAGATCCTGAGCA
TTCAGCTCCTGTCTTACACAACAGACACCCTCAGTCCCATCAAAGCCTGTGAAGTTT
CCCTACATCCACCATTGAGACATATTCCAGAGCAGCCTCTCAAATTCGCTTAACAGGAT
GGGACACGATATGGTGGAGCTCCTGGCTCAGGACAGCTGCCTCACCCCTTCTACTGAGA

26321 CCCCTTCCTACTGAGAAGTCTGTATCTGCTGGTTAGAGCTATCAAAGTGTAGAAGGCTTA
GTGCCTGTCCCAGCAAGTGTCCCCTCAAAGCCTTCTTGTCTTCTTCTTCTGAGAAAA
GCATACAAGAATGAGACCTTCTATGTTAGAGAGAACTCAGCCTCCACTCTCAATTGACTT
GGTTGACTGATGAATTGATGCCCTGAGGAGGGGATAGATTGAGGGAAGAGACTGTGCTGA
ATGAGTCTGTGTTTTCTAGCTTTGCTGTCTGTGCAAATAGTGAACCCAGAAAAATATC
[G, A]
GGTGGTAGACACACAGACACTCTAATTGTCTGAATTTAAATATTATTAAATGGAACCTTA
TAGTATCATATATATTGATACCATAATATCACATAAAATTTGTTTGATATATAAACA
TATTGATATTTTATCATATAATATCATAAAGCAGTTGTGCACACAATAGCAGATAATATTCT
CCGGTTCTATAAAGTTTATATGTTAATGTTCTTACAAAATTTAACTCAGTTATTTTATAA
AATTACCTAACAAAATTTTGTACTGTGCTATCATAATAATACATAAACTATGAAATCA

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53101 ACCAAGGCCATATTGTGATTTAAGAACTAGCAGACAGGACTTTC AATTGACTTGATATG
ATTTATTATTTTTACTACTTATAAGAATGGAATAAGTTCTCCTTAGTTTTTTCTTGGA
GAAAGTCTGACATGTGAGGCACAGATGAGTTATTAAGGCAGATGACTTTCCAGCCTTGT
CTTAAATGTTCCATTCTTTACCTTAGAAATTATTTAAATTTGTGTCTTCCAAATACTGTA
GTAATATTGATGCTCCAAAGAGATGTCCACGGAGATTCTGCTCTTGTGTGTCCACCCTG
[G, C]
AGGGAGCTGAGGCAGTTTCTTATGACAGTTTCAGAAGCGAGTAGTCGTGCAGTACTTAAT
CTAAAAAACTTAATGGAACATGAATTAAGAGAATGATCACTGTTTAGTTCTATCAGCAA
ACTATTAAAAGTGATCCAAAGGAGGTATTTATAAAGAGATATTTAAAGATTTTTCAAGGG
AGCCTTATTAGGGCAGAAACGCAGACACTATCGCTGACCTCACCACAGAAAATACCCTC
ATGGGTTGGGAGGGACCAAGGACGCTCTGGTCTGCTGACCTGCATTAATCACAGCCAG

54556 GAAAGGGAGGAGCGAGAGAGGGCTGGGGCTGAGGAGGAGGCTGTGTGAGAAAAGGGCGGG
GCGCGCCCAAAGTCTGGCGGAAGAGCGTTACCCTGGCAACCCTCCCGCGGAGGCCGAGAG
AGGCCACCGGCCCTTTGTTGATCTGCGAGAAATCAAACACGACAGCAAGCATTAGC
CTGCAGCTCGAGGAGACAAGGTGTCACAATTACAAGGGGAACTAGCCGCCCTAGCTCCA
CTGTCTCCCCAGCACGAGAGATTTGAGAACAGAAAGGCTTCCCTCCGCGAGGGCGAAACTG
[G, C]
TGGGCTGCCTGGAAGGGCGAGGCAGGGAGCGGAACCGTCTTCAGGAAATTTTCGGGAGTTC
CGGGGTCAGGTCCACTCCCCGGCTGTTGTTGTGTTGTTGGCAGGGCAGAGGGTCTAGGAT
GCCAGCCTGCTCCGGGCTGCGCTGTGCGCCTATCCAGGGCGGGGGGATGCGGGGCGACA
CCCCGCTCCCGGTGCATCCAGGAGTTGTAGTCTCTTCACCGGTTCCCCACTGTGGGTGGT
GGGGCTGCAGGAGGACAATTC AATTGAGATAGGAGCGGAGGCGGAGCGCGGCCGTGCAG

61872 ACACTTCACATCAGGGTTCCCAAATGTATAAAGTTAACATTGACACAAATGAAGAAGGAA
ATGGCTATGCAAAAATAGTAAGAGACATAATTACCCACTACCCACTATCAGTAATGAAT
AATAAAGCCAGACAGAAAGTTAACTTGAGAACAGAGAATTTGAATAACACTGCAAACTCT
AAACCTAACAGACATATAGAAAACACTAGTCACAGTGAATAGAAGTGA AAAAACAAAAGA
AACAAACACTCCACACAGCAATATCAGAATATACAATTTTTTCAATAGGT CATGAAACAT
[-, T]
CTCCTGGGTTGATGACCTACTAGGACACAAAACAAGTTTTGCTAAATTTTAAATGGTAA
AATATGGGCCAGGGATGGTGGCTCATGTCTATCATTCCAGCATGTTGGGAGGCTGAATTG
GGAGGATTGAGTGAGTTTAGGAGTTCATGGCCAGCCTGGGCAACATAAGGAGACCTTGT
TTTACAAAATATAAAATTA AAAAATTA ACTGGGCATGATTACACGTGCCTGTGTGCCAG
CCACTCAGCAGGCTGAGGTGGGAGGATTGCTTGAGCCTGGGAGATCAAGGCTGTGGTTAG

62172 TCTCCTGGGTTGATGACCTACTAGGACACAAAACAAGTTTTGCTAAATTTTAAATGGTA
AAATATGGGCCAGGGATGGTGGCTCATGTCTATCATTCCAGCATGTTGGGAGGCTGAATT
GGGAGGATTGAGTGAGTTTAGGAGTTCATGGCCAGCCTGGGCAACATAAGGAGACCTTGT
CTTTACAAAATATAAAATTA AAAAATTA ACTGGGCATGATTACACGTGCCTGTGTCCA
GCCACTCAGCAGGCTGAGGTGGGAGGATTGCTTGAGCCTGGGAGATCAAGGCTGTGGTTA
[G, C]
CCATAATTGAGTCACTGTGCTTCAGCCTGAGTAACATAGCAAATCTCTGTCCCAAAAGAG
ATTAAAATATTACAACTATCATTTTTGATTAAAGGGAATACAATGAGAAATCAATAGC
AGAAAAAATACTGGAAATCTACAAATATGTGGAATTAACAACCCACTCTTCAGCATG
CTCTCGTTAAGGGTCGGAAGACAATATTGTGAAGATGTTACACTACCCAAAATTATCTA
CAGATTCAATGTGATCGTGTCAAATTTTAACTGTCATTTTATTTGCAGAAATACAAAAA

62860 TGACTTCCTAATGTATTACAAAACCTACAGTAACCAAATATTTGGTACTGACATAAAGGC
AGACAGACAGACCAATGGAACAGAATAGATCACAGGAATAAAGTGCATATATATGGCCA
AATGAGGAGTTATTTTTATATCCATATTCATTGCAGCATTATTCACAACAGCTGATAGGT
GGAAGGAACCCAAATGTCCTCAGTGAATGAGTGGATAAAGGCAATTTGGAATATACAAA
TAATGGAATATTATTCAGTTTTTTAAAGCAGGAGATCTGATTATTTTACACTAAGAAT
[A, C]
AATCTTGAGGACATTATGTAATGAAATAAACCAAGTCACAAAAGGACAGACACTGTTTGA
CTCCAGTTAAATAAATATCTAATGTAGTTAACTCTTAGAAACAGAAAGTAGAATAGTA
TCAGTCAGAGCCTTAGGGGTGGAATAAAAGGAGTAGTTGTTGTTTCATAGGTATTGAATT
TTAGTTTACAAACATAAAATCATTTTAGCGATATGTTGCATAGCAATGTGAATATATTTA
ATATTATTTAACTATGTACTTAATATATTTAAGATGGTACATTTTATGTGTTTTGAGTAC

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67086 AGGATATATGGGATTAATTTTGGGTAAAATCCATCTCAACTTACAGGACATTACTGTAGT
CCCAGGAGTTGTTGACTGTGATTATGAAGGAGAAATCAAGTAGTGGTAATATCACAAGA
TTTGTAGTTTTTGAACCTGGAGAATATGTAACCTCACTACTGCTTATCCCTGGGAGTT
GTTTCCTTCTCCACATAAGGAGAAATGAGAGAATCAAGGATTTGGGAGTACAGCTAGGAG
GAAAATTTATTTATCACAACCCATAGCATCTAATAGACCCACCTGTACAGTGCAAATTA
[C, A]
GGAAAAAATTTCTATGGGCTTATGGATATGGGAGCTGATGTGTGAGTAATATCTAAAA
CAATTGGCCCCCATCCTGGCCCTGCAATTAACCTCTACATCGCTAGTGGGAATAGGAAC
AGCTCAAAGTGTTCACAGAGTGTGAAATTTTACCCTGTCTCAAACCAGATGGACAGTC
ATGTACTTTTAAAAATTTATTTTGCAAATGTAACCTGTTAACCTATGGGGCCAAGATTTACT
TACAGCATGGGATATAAGACTTGCAAATGAACTATTGACAATCCAGGGTTCAAAATGTT

67621 TTTACTTACAGCATGGGATATAAGACTTGCAAATGAACTATTGACAATCCAGGGTTCAA
AATGTTAAAGAAAAATGGGATGTGAGGCAGAAAAGGCTTAGAAAAAGTCCCTACAGGGAAAC
ACTGATCCTATATCAATAGCTGGGCAACAGATAGAAAAGGGCTAGGTCATCAGAATTC
TGATGGGAGTCACTGATATTTCTCCCCATCTACTGTTTTACCCTGGAGTGGCTGACTA
AAAACTGTATGGGTGGATCAGTGGCCCTATCACAGGAGAACTAACACAATTCATC
[A, C]
GCTAGTAAAAGAGCAAATGGATGCAGGACATATTGAAGAGTCAGTTAGCACCTGGAATTC
ATCAGTATTTGTAATTCCTAAAAAGTCAGGAAAATGATGACTGCTACATGATTTGAGAGC
TATTAATGCACACATTAACCAATGGGTGCATTACAGCAAGGTCTGCCATCCCCGGCAGC
CTTTCCAGGAGGCTGGCCTCTCAAAGTAATATATCTTAAAGATTTTTTATTTATTTTTT
ATTTTACTGTTACATGAGCAGGATAAGCATCGATTTGCCTTTTATGTGCTTTCTGTTAAT

70582 TGTAATATCCTGTGCAGTATGATTTTTCTGTGCAGAAGCAAAAACATATTGGGCATATTT
TCCTAACCCACCGTAGTGTGATCATACTCTGAAGCAGCACTCCTCCTGAGATATATCAT
GATCAAGGAGCATCAGTACCAGGACCTCTAACTCCCCCTGACACAGAGCAATTAGACTCT
CATAACAATGGTATCAATTATACCACTCCATTTGGAGGGACTTCCTTTATGTGTACCCAG
GATACATTGCTCAACTGCAGTTGCCTTGCAGTTTGATCCCAAGCATGGTTGAGTTACCAT
[A, T]
AAAAAATATGTACCTATTAGACCTTAGCTTTATTAATATTACTTGTGTAGTTACTAATC
ACTCCTGGCCCCCATCACCCAAATGTACTGATTATACAGAATGGGCTCCCTTTGATAATT
CTCACCCCCCTCCTTGGGCCCCTGTCTTGGCCCCCTTAGCTAGACAATAGTCCATGTTAA
TGGGAGACATTATTGACTGGGGTCCCTGTGGTCATTAAGATGGGAGAGATGAGAATCAGA
CCACATGGCATAAACTTCACTGGCACTGGTGGCGAACTTTAACATCTCTTCACTTCAAC

74175 GCTGCGCCTGCAGCCCCACTGAGCGTCGGACTCCTTCCTGGAGTAGGGAGGTCTCTGTT
CTTCTGGAGCGACAGACACCCTTCTCCTGGCCTTCTCGCTTACTAGCCCGGCAGGTGCT
GGACAGGAGATCTGAGCTGGTCTGCGTCTCTGAGGAGCTAGGAGCCCGGCTGGGAGAAC
AAGGAGACGAACCTGTGGGAGAAAGGGCGACAGGAACGCCAGGCTCATGGGACCGCTGGC
AGCGGCTGGGTATGGCTGGCGGCTGAATGGTCAGAGATACGAGAGGTGGCCACTGTCCC
[C, -]
ACCTTTGGCCCCCTAGCCGGCATTCGTACATTCTGTGCTCAACAAACGGAAGCGGCAGCT
GGAGCTGCTGCTCCGGGAGGTGGAGTGGCCTGGCAGAGGGCACATGGCTGCCACCTGCTG
CAAGGTGAGCTGGTCTGCAGCCTGGGCCCACAAAAGGCCGCTCTTGTGCAGGACACACCG
CTGCCCTTGACCCTCTTGTCTCCCCGCTGCTGTGCAAAATGCTCAGGTCCCTGATCTCG
GGCTTTCCTGGCAAGTGCACCTGTGGTGGGAGGCAGCAGGGAGGAGGGCTTTCCAGGAG

74478 CTTTGGCCCCCTAGCCGGCATTCGTACATTCTGTGCTCAACAAACGGAAGCGGCAGCTGG
AGCTGCTGCTCCGGGAGGTGGAGTGGCCTGGCAGAGGGCACATGGCTGCCACCTGCTGCA
AGGTGAGCTGGTCTGCAGCCTGGGCCCACAAAAGGCCGCTCTTGTGCAGGACACACCGCT
GCCCTTGACCCTCTTGTCTCCCCGCTGCTGTGCAAAATGCTCAGGTCCCTGATCTCGG
CTTTCTGGCAAGTGCACCTGTGGTGGGAGGCAGCAGGGAGGAGGGCTTTCCAGGAGCC
[T, C]
TGAACAGAGGATCTTGGCATAAAGAGGAGAGAGAGGTGGCTGACTGGTTCCACTTGTAGG
TAGGGGGGCAACAAACCCCATGGGACCCTGTTTTTTCAGGGAGATTTCACTTCACTTCTT
ATCTTTTCTCCACCCACTTGAGCCTCTGAGAATAGAGGAGACGAGGCTGTTTAAATTGG
CCTAACCATATGGTCTGGACCTTGCCCCAGGGCAGACCTAATTTTGGGGCTCTTTGCA
GCATGGAGGCTCACGCTGTCCACCCAGGTGTCTTCAATATAGGGTCTAGTTAGGCCTG

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77092 TGCAGAATGCAGATGGATCCAAAAATCACAGGATGTGGGAGGTGAAGGAAGAGCTTGTA
 AAAATGAAAAGTGGCTGGTGAAGAGTAGGAGGCATGAAGAGGATGAGACCTGCCTGGGG
 CAGTGCACATGTTTTGTTCCAGCCAAACAATCAGATGAGGTCTTGGTCTTGGACCTGGTG
 CCAGGGAATTCATAAGCCCCCTTTTGCTGTGGCCTGGGAGCTGAGGTCTTTGGTTCTGAA
 ACCAAATGTAAATTTTGACTCTGGAATACCTGTCTGTTTAACCAAGTTTCTCTCTACTGG
 [T, G]
 GATCGCAGGAAATGAATTATCCTGTAAAATTTTGTGGATTCTTCTCAAAGGCTTCAATGA
 GTACACTGATTTGTGGTTCAGTGATGGATGTCCCTTTCCTCCTGCCTTCTTATTTGACTT
 ACACCATCAATATTAACATATGGCAGTTATGGTAATATCATTCTTTACAACAGAGGAACT
 TCAAGTCATTCATTGATGATATCAAAGCCTCATTCTCCTACATTAAACATTCTCCTACAT
 TTAGCTTCTTGAATCTTCTATGTCCACTGTCTAGAAAACCTAAACACATGAAGTACCACA

77328 TGA AACCAAATGTAAATTTTGACTCTGGAATACCTGTCTGTTTAACCAAGTTTCTCTCTA
 CTGGTGATCGCAGGAAATGAATTATCCTGTAAAATTTTGTGGATTCTTCTCAAAGGCTTC
 AATGAGTACACTGATTTGTGGTTCAGTGATGGATGTCCCTTTCCTCCTGCCTTCTTATTT
 GACTTACACCATCAATATTAACATATGGCAGTTATGGTAATATCATTCTTTACAACAGAGG
 AAACCTCAAGTCATTCATTGATGATATCAAAGCCTCATTCTCCTACATTAAACATTCTCC
 [T, C]
 ACATTTAGCTTCTTGAATCTTCTATGTCCACTGTCTAGAAAACCTAAACACATGAAGTAC
 CACAAACTAGAAATAAATACCTCAATAGGCACCAATCATAAAAGTAAATCCAAGAAGGAA
 CAGAATATATGAATACATATATAACAAGTAAAGGGATTCAATTAATTAATAAATCATCACA
 CACAAAAAGCCCAGAGTCATGTGGCTTAACTGATAAATTCTACTAAACATTTAGTGAAG
 AATTAATGCCAACTCTTCACAAGGCCCTCCAGAAAATAGAAGACAGTTATTGGGAACACT

77385 CTACTGGTGATCGCAGGAAATGAATTATCCTGTAAAATTTTGTGGATTCTTCTCAAAGGC
 TTCAATGAGTACACTGATTTGTGGTTCAGTGATGGATGTCCCTTTCCTCCTGCCTTCTTA
 TTTGACTTACACCATCAATATTAACATATGGCAGTTATGGTAATATCATTCTTTACAACAG
 AGGAACTTCAAGTCATTCATTGATGATATCAAAGCCTCATTCTCCTACATTAAACATTCT
 TCCTACATTTAGCTTCTTGAATCTTCTATGTCCACTGTCTAGAAAACCTAAACACATGAA
 [G, A]
 TACCACAACTAGAAATAAATACCTCAATAGGCACCAATCATAAAAGTAAATCCAAGAAG
 GAACAGAATATATGAATACATATATAACAAGTAAAGGGATTCAATTAATTAATAAATCATC
 ACACACAAAAAGCCCAGAGTCATGTGGCTTAACTGATAAATTCTACTAAACATTTAGTG
 AAGAATTAATGCCAACTCTTCACAAGGCCCTCCAGAAAATAGAAGACAGTTATTGGGAAC
 ACTTCCCAATTTGTTCTATCAGGCCAGTATTACCCTGATACTAAAGCCAGACAAAAGCAT

77947 GGCCAGTATTACCCTGATACTAAAGCCAGACAAAAGCATCACAAGTAAATATGAACATAG
 ATGAATTTCCCTGATAAATACACAAACAGAAAATCTCAAAAAAGAGTGAAATGAATCAAG
 AATAAATCAAATGACTGTACACCATGACCAAATGGAATTATTTACAAATGCAATATTG
 ATCTATCCAATAATCAATCAATGCATTACACAAAGTAATAGGATAAAGGAAATTAACAGA
 AAGGTCTTTCAACAGACACAGGGAGCATTTAACCAATCCAATATTCATTACAGATCTCC
 [C, T]
 TGGAAAAGAGGAGTACAAGAACTTCTAGATCTGCTAAAAGGCGTCAATGTAAACTTA
 CAGCTAACCCCATATAATAAATACTGGTTGTTGTGTCTTGACATTTGAGAACAGACA
 AAAATGTTAACATCCAAATAAATTACATAAGAAAAATAAACAAATCATCAATGTGGGAA
 AATAAGAGGTTAGAACTCTCTATCATTGCAGAGGACATAATGTGAATATAAAAGTTTATA
 AGAAATTCATTAAACTCACTACAACCAATAAGTGAGTTCAGCAACATCACAGATACAA

79395 CTGAGCATGGTGACATAGGGCATGCCATTGACACCCAATTTGCTGGTGTTCACCTCCACA
 TACTAAGTTGCTAGAGAATTTGCAGTGGATTTCCATTTTGCTGCATCTGGCTGTCCAGAA
 GCCCTGCAAGTAGAATGGGATGGTCAGGAGAAAACATTGAAAGAATAGATGGGAGTTTCCAG
 AGGCTGCCCACCTCCTGCCCTCTGCCACGGGCCACAGCCCTCACCCAGCTGTCCAGTG
 TGTATGCTGCTAAAGGCTGCTGCACCTTGTCTCCATCACAGAGGTGGGGTGACAGCAGT
 [G, C]
 TGTGGGCACCACACTCCATGATCAGCCTCTACTGTTGGTGCCACAGCTCCAGGTAGAAGG
 GCAGGTGAGCCAAAGACAGGTCCCACCTTCCACATCCAGCCACATTCCCACCAACTTCC
 AGGCCACCTCCATATGCTGATGTGATGCTCTCCTTAGAGCTCTTGTGGTTCTTCAGCCA
 GGAGATGGAGAGAGTGGGGTTTCAAGAGTAAGGCAGTGAAAGTTGGTTTGGGTGGCCACC
 ATGGTTGGTGGTTTCTGTCCATCCACTCGGTCCAAGTCCAGTAAGGGGCCCTCTGCTGGT

81111 ACTAGGGTGTGTGGGCAGGGGCAGAGGCCATTGAGGCAGGTGAGGAGAAATTTTCATCCT
 CTCCTGGTCTGCCCCTCTCCTGGGGTCTAATTTCTCTATTCCGTCTGCCTCTGGGCTCC
 CTGGCTGGCTCCTCTTCACTCTTTGCTGCTCAGCCAGAGGTCCCAGGGGCTCAGCCC
 ACCACAAATGGTCCCAAGTTGTAGCTGACCCTTCCATGTCCATCCCATGAGGACCCCTCA
 TCTGCCTGAGTATATCTCTGGGCTCCTCTGAAACCAGAAGTCCCACCTCACTGACTGCTC
 [-, C]
 ATGGCTAGGCAGCATCCACCTGCCACTGTTCCAGGCCAGAATGACTGGGCATTGTCCCCC
 TGCTGCTCCCTCACACCTACAGCTCATGCCCCAAAATGCTGTTGGCATCCTTCATACA
 ACCCTCACAGCCACCCTGCCCCCTGCTGGGCTGTAGGTTTGGTCTCCTGGTGCCTTAACC
 CCTTGTCCATCTGCCCCCTGGGCAGCCACCTGAGCCCCTGAGCACTGCTGTGCTCACATG
 TGCAGTAGCCCCCTCACCCAGAGCCAGCATCGAAGTCTCCACAGGCCAATTCTGGCCTCA

81610 TGGGCAGCCACCTGAGCCCCTGAGCACTGCTGTGCTCACATGTGCAGTAGCCCCCTCACC
 CAGAGCCAGCATCGAAGTCTCCACAGGCCAATTCTGGCCTCATCACTGCTCCTGGAACCC
 CAGGGCCCTGTGCCCCAATCTCCCCATCTGCAGCATGGGTGTCTCTTCTACCCCAAGCC
 TGCCCCCAGAGCTCAAGACATCCAGAGCCATCTAATACATATGTAATACATACAAATTA
 CATAACAATTTGTAATATGTTGTACTACATACACATTTTCATATGAATTCATCATAATAC
 [G, A]
 TACAAATTATGATGTCATAATATATTGTGATGTGACAATACACATGAATTATCATGTCAT
 AATACATTGTGATGTCATAACACATACTAATTATGATGTCATGATATATTGTGATGTTAT
 AATGCATATGAATTATGGTGTGACAATACATATGAATTATGATGTCATGATACATTGTGA
 CGTAATAAGAATTGTGACATCATAATATATCATGATGTCATATGCATGCAACTTATGATG
 TCATGATATACTGCAATGCCTTAATACAAACCAATTATGATACAGTAATATGTTGTGATG

Map data:
 chromosome 16